STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: [redacted]

TO:	From:
Robert Mondesi Location: cm-1/5d169b01 Art Unit: 1653 Friday, June 27, 2003 Case Serial Number: 832501	Toby Port Location: Biotech-Chem Library CM1-6A04 Phone: 308-3534 toby.port@uspto.gov

Search Notes

Dear Examiner Mondesi,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact ***the searcher or contact:***

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

- *I am an examiner in Workgroup:* ☐ *Example: 1610*
- *Relevant prior art **found**, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
  (journal articles, conference proceedings, new product announcements etc.)

- *Relevant prior art **not found:***
  - ☐ Results verified the lack of relevant prior art (helped determine patentability).
  - ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library.CM1 – Circ. Desk

STIC-Biotech/ChemLib 94570

From: Mondesi, Robert
Sent: Thursday, June 26, 2003 3:18 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

My Name Robert Mondesi
ART UNIT is 1653
Phone # 305-4445
Room number 5D16
Examiner number 79912.

please perform a sequence search on SEQ ID NO : 18 of patent number 09832501.

Thank you.

OM protein - protein search, using sw model

Run on: June 27, 2003, 16:58:25 ; Search time 74 Seconds
(without alignments)
1053.400 Million cell updates/sec

Title: US-09-832-501-18
Perfect score: 3103
Sequence: 1 DAHKSEVAHRFKD[illegible]ENFK .... [illegible]FAEEGKKLVAASQAALGL 585

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: [illegible]8470 seqs, [illegible] residues

Total number of hits satisfying chosen parameters: [illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: [illegible]:*
2: [illegible]:*
3: [illegible]:*
4: [illegible]AA1983.DAT:*
5: [illegible]:*
6: [illegible]:*
7: [illegible]:*
8: [illegible]:*
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21: [illegible]:*
22: [illegible]:*
23: [illegible]:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3103	100.0	585	10	AAP[illegible]	Mature human serum
2	3103	100.0	585	11	AAR[illegible]	Human serum albumi
3	3103	100.0	585	11	AAR[illegible]845[illegible]	Human serum albumi
4	3103	100.0	585	1[illegible]	AAR80[illegible]	Human serum albumi
5	3103	100.0	585	18	AA[illegible]20111	HSA protein sequen
6	3103	100.0	585	21	AAY[illegible]487[illegible]	Amino acid sequenc
7	3103	100.0	585	21	AAY8[illegible]	Yeast codon biased
8	3103	100.0	585	22	ABB7[illegible]	Human mature album
9	3103	100.0	585	22	AAE13399	Human albumin (HA)
10	3103	100.0	585	22	AAM52567	Mature human serum
11	3103	100.0	585	2[illegible]	AAP[illegible]	[illegible]
12	3103	100.0	585	22	AA[illegible]21[illegible]	[illegible]
13	3103	100.0	585	2[illegible]	AAP[illegible]	[illegible]
14	3103	100.0	585	2[illegible]	ABD[illegible]	[illegible]
15	3103	100.0	585	23	ABD[illegible]	[illegible]
16	3103	100.0	585	23	AB[illegible]3047	[illegible]
17	3103	100.0	585	23	AAU75220	Mat[illegible]
18	3103	100.0	609	21	AAB36542	R[illegible]
19	3103	100.0	609	21	AAB36549	R[illegible]
20	3103	100.0	609	21	AAY[illegible]17	[illegible]
21	3103	[illegible]	[illegible]	21	AAB[illegible]	[illegible]
22	3103	[illegible]	[illegible]	21	AAB[illegible]	[illegible]
23	3103	[illegible]	[illegible]	21	AAB[illegible]	[illegible]
24	3103	[illegible]	[illegible]	[illegible]	AAB[illegible]	[illegible]
25	[illegible]	[illegible]	[illegible]	[illegible]	AAB[illegible]	[illegible]
26	[illegible]	[illegible]	[illegible]	[illegible]	AAB[illegible]	[illegible]
27	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	[illegible]
28	[illegible]	[illegible]	[illegible]	[illegible]	AAW[illegible]	Mat[illegible]
29	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	[illegible]
30	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	[illegible]
31	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	[illegible]
32	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	[illegible]
33	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	[illegible]
34	[illegible]	[illegible]	[illegible]	[illegible]	AAW1[illegible]	[illegible]
35	[illegible]	[illegible]	[illegible]	[illegible]	AAY[illegible]	[illegible]
36	[illegible]	[illegible]	[illegible]	22	AAB[illegible]	M[illegible]
37	[illegible]	[illegible]	[illegible]	[illegible]	AAW[illegible]	[illegible]
38	[illegible]	[illegible]	[illegible]	[illegible]	AAW[illegible]	[illegible]
39	[illegible]	[illegible]	[illegible]	[illegible]	AAW[illegible]	[illegible]
40	[illegible]	[illegible]	[illegible]	[illegible]	AAW[illegible]	[illegible]
41	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	S[illegible]
42	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	Hum[illegible]
43	[illegible]	[illegible]	[illegible]	[illegible]	AA[illegible]	[illegible]
44	[illegible]	[illegible]	[illegible]	[illegible]	AAB[illegible]	H[illegible]
45	[illegible]	[illegible]	[illegible]	[illegible]	AAW[illegible]	Human [illegible]

ALIGNMENTS

RESULT 1
AAP[illegible]
ID AAP[illegible] standard; protein; 585 AA.
XX
AC AAP[illegible];
XX
DT [illegible] (first entry)
XX
DE Mature human serum albumin [illegible]
XX
KW Human serum albumin, [illegible]
KW plasma expander.
XX
OS Homo sapiens (Human).
XX
PN [illegible]
XX
PD [illegible]
XX
PF [illegible]
XX
PR [illegible]
XX
PA (DELT-) DELTA [illegible]
XX
PI Ballance [illegible]
XX
DR WPI; 1990-[illegible]
DR N-PSDB; AAN[illegible]
XX
PT New N-terminal fragment of human serum albumin [illegible]
PT [illegible]
XX

```
PS   Disclosure; Fig 2; 20pp; English.
XX
CC   Mature protein of human serum albumin (see corresp. AAN?????).
CC   Used to make new N-terminal fragments which are used as plasma
CC   expanders, or as substitutes for HSA or BSA, in tissue culture
CC   media.
XX
SQ   Sequence   585 AA;

  Query Match             100.0%;  Score 3103;  DB 10;  Length 585;
  Best Local Similarity   100.0%;  Pred. No. 1e-254;
  Matches  585;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60

Qy         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120

Qy        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180

Qy        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240

Qy        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300

Qy        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360

Qy        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 420

Qy        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

Qy        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540

Qy        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
              |||||||||||||||||||||||||||||||||||||||||||||
Db        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585


RESULT 2
AAR05318
ID   AAR05318 standard; protein; 585 AA.
XX
AC   AAR05318;
XX
DT   08-OCT-1990  (first entry)
XX
DE   Human serum albumin gene product.
XX
KW   Human serum albumin; HSA-A; yeast; ds.
XX
OS   Homo sapiens.
XX
PN   JP02117384-A.
XX
PD   01-MAY-1990.
XX
PF   26-OCT-1988;   88JP-0268302.
XX
PR   26-OCT-1988;   88JP-0268302.
XX
PA   (TOFM ) TOA NENRYO KOGYO KK.
XX
DR   WPI; 1990-176228/23.
DR   N-PSDB; AAQ04779.
XX
PT   Human serum albumin prepn. by yeast host -
PT   by culturing transformed plasmid yeast to produce serum albumin
PT   removing it.
XX
PS   Disclosure; ?pp; Japanese.
XX
CC   Mature HSA-A may be produced using the sequence incorporated into a
CC   plasmid ... with suitable controllers, and transferred to a yeast
CC   expression system.
XX
SQ   Sequence   585 AA;

  Query Match             100.0%;  Score 3103;  DB 11;  Length 585;
  Best Local Similarity   100.0%;  Pred. No. 1e-254;
  Matches  585;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60

Qy         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120

Qy        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180

Qy        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240

Qy        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300

Qy        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360

Qy        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 420

Qy        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

Qy        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540

Qy        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
              |||||||||||||||||||||||||||||||||||||||||||||
Db        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585


RESULT 3
AAR08457
ID   AAR08457 standard; Protein; 585 AA.
XX
AC   AAR08457;
XX
DT   16-APR-1991  (first entry)
XX
```

```
DE   Human serum albumin.
XX
KW   HSA; binding; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          123..303
FT                   /label= A
FT   Region          1..303
FT                   /label= B
FT   Region          123..585
FT                   /label= C
XX
PN   [illegible] A.
XX
PD   2? APR 1999.
XX
PF   10 SEP 199[illegible]  [illegible]
XX
PR   [illegible] 199[illegible]  [illegible]
XX
PA   ([illegible]) [illegible]
XX
DR   WPI; 199[illegible]/42.
DR   N-PSDB; AA[illegible].
XX
PT   New human serum albumin fragments - used to bond medicines and for
PT   stable folding of protein(s).
XX
PS   Claim 1; Fig 8; 24pp; Japanese.
XX
CC   Fragments A-C of HSA are expressed as fusion proteins with the
CC   signal peptide of E. coli alkaline phosphatase. The fragments are
CC   selected for their specific properties. The C-terminal truncated
CC   fragment, B, does not bind long chain fatty acids but does bind to
CC   various medicines at the central region. The N-terminal truncated
CC   fragment, C, has good stability in protein folding. The central
CC   segment, A, has characteristics of both B and C.
CC   See also AAQ[illegible] Q[illegible].
XX
SQ   Sequence  585 AA;

  Query Match             100.0%;  Score [illegible];  DB [illegible];  Length 585;
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches  585;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60

Qy         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
Db         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120

Qy        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
Db        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180

Qy        181 K[illegible]KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
Db        181 K[illegible]KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240

Qy        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA [illegible]
Db        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA [illegible]

Qy        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
Db        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360

Qy        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 42[illegible]
Db        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST [illegible]

Qy        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEK[illegible]
Db        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEK[illegible]

Qy        481 [illegible]
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Qy        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
Db        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585


RESULT [illegible]
AAR[illegible]
ID   AAR[illegible] standard; protein; [illegible] AA.
XX
AC   AAR[illegible];
XX
DT   [illegible] JAN [illegible] (first entry)
XX
DE   Human serum albumin.
XX
KW   Serum albumin; HSA; aspartyl protease; [illegible] Yap3[illegible];
KW   Saccharomyces cerevisiae.
XX
OS   Homo sapiens.
XX
PN   WO9[illegible] A1.
XX
PD   [illegible] SEP 199[illegible].
XX
PF   01 MAR 1995;  95WO-[illegible].
XX
PR   0? MAR 1994;  [illegible].
XX
PA   (DELT-) DELTA BIOTECHNOLOGY [illegible].
XX
PI   Gilbert [illegible], Kerry W[illegible];
XX
DR   WPI; 199[illegible].
DR   N-PSDB; AA[illegible].
XX
PT   Yeast with reduced [illegible] aspartyl protease [illegible]
PT   [illegible] - used [illegible] human serum albumin without [illegible]
PT   [illegible] fragment
XX
PS   Example [illegible]
XX
CC   The cDNA [illegible] AA[illegible] encodes HSA (AAR[illegible]) [illegible]
CC   [illegible] directed [illegible] to [illegible] the [illegible]
CC   [illegible] in the [illegible] albumin fragment [illegible]
CC   when the cDNA is expressed [illegible]. Mutations [illegible]
CC   [illegible] V[illegible] [illegible]. The latter [illegible]
CC   mutations, especially, improved stability of HSA to yeast [illegible]
CC   proteolytic [illegible], allowing increased prodn. of [illegible]
XX
SQ   Sequence  585 AA;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEV[illegible]
Db          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEV[illegible]

Qy         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHK[illegible]
Db         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHK[illegible]
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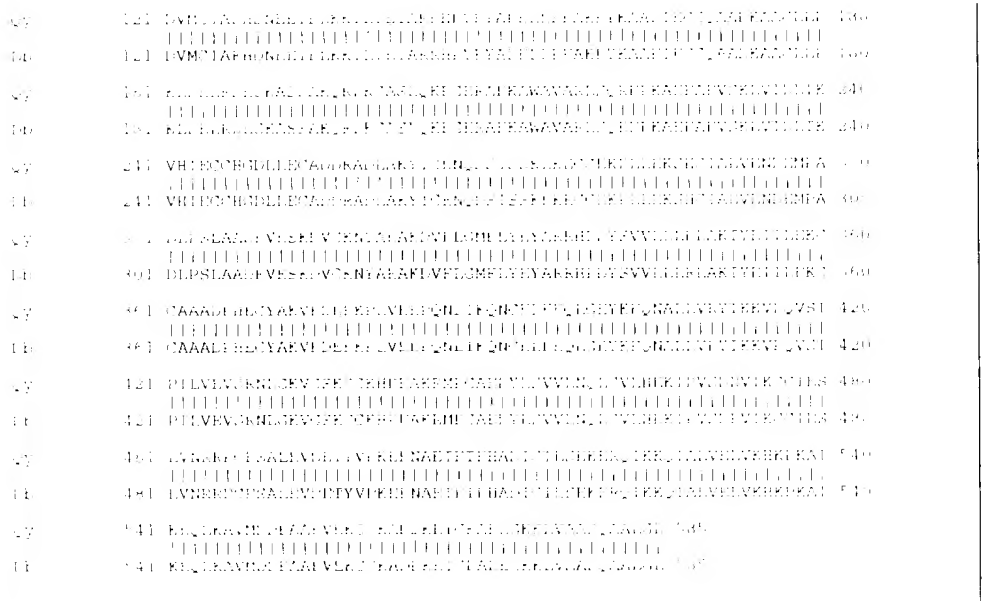

RESULT 5
AAY84847
ID AAY84847 standard; protein; 585 AA.
XX
AC AAY84847;
XX
DT 08-AUG-2000 (first entry)
XX
DE Amino acid sequence of a human albumin protein.
XX
KW Human; albumin; ischaemic state; serum protein; metal ion binding;
KW perioperative ischaemia; ischaemic myocardial infarction;
KW progressive cerebral artery disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified site 1
FT /note= "glycosylated and oxidised"
FT /label= 1
XX
PN WO200049048-A1.
XX
PD 17-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US02507.
XX

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PR   [illegible] 1998;   98US-[illegible].
PR   02-OCT-1998;   98US-0165541.
PR   02-OCT-1998;   98US-0165926.
PR   11-JAN-1999;   99US-0115392.
XX
PA   (ISCH-) ISCHEMIA TECHNOLOGIES INC.
XX
PI   Bar-Or D,  Lau E,  Winkler JV;
XX
DR   WPI; [illegible]/26.
XX
PT   New method for the continuous detection of ischemic states comprises
PT   detecting and quantifying the existence of an alteration of the serum
PT   protein albumin
XX
PS   Disclosure; Page 97-100; [illegible]pp; English.
XX
CC   The present sequence represents human albumin protein. The specification
CC   describes a method for the continuous detection of ischemic states. The
CC   method comprises detecting and quantifying the existence of an alteration
CC   of the serum protein albumin. The method comprises contacting a
CC   biological sample containing albumin from the patient with an excess
CC   quantity of a metal ion salt, where the metal ion binds to the N-terminus
CC   of naturally occurring human albumin, to form a mixture containing bound
CC   metal ions and unbound metal ions, and then determining the amount of
CC   metal ions bound to the albumin N-terminus. The amount of bound metal
CC   ions is correlated to a known value to determine the occurrence or
CC   non-occurrence of an ischemic event. The methods are useful for detection
CC   of ischemic states. The methods are also useful for distinguishing
CC   perioperative ischemia from ischemia caused by , amongst other things,
CC   myocardial infarctions and progressive coronary artery disease.
XX
SQ   Sequence   585 AA;

  Query Match            [illegible]%;  Score [illegible];  DB 21;  Length 585;
  Best Local Similarity  100.0%;  Pred. No. [illegible];
  Matches  585;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60
Db          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60

Qy         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
Db         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120

Qy        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
Db        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180

Qy        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
Db        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240

Qy        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
Db        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300

Qy        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
Db        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360

Qy        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 420
Db        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 420

Qy        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
Db        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480

Qy        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
Db        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
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```
Qy        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
Db        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585


RESULT 7
AAY83946
ID   AAY83946 standard; Protein; [illegible] AA.
XX
AC   AAY83946;
XX
DT   2[illegible]-2[illegible]  (first entry)
XX
DE   Yeast codon biased recombinant human serum albumin protein.
XX
KW   Recombinant human serum albumin; HSA; yeast; [illegible]
KW   overlapping oligonucleotide; [illegible]
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   CN1240[illegible]-A.
XX
PD   22-DEC-1999.
XX
PF   17-JUN-1998;   98CN-[illegible].
XX
PR   17-JUN-1998;   98CN-[illegible].
XX
PA   (HALT-) HALT[illegible] BIOENGINEERING [illegible].
XX
PI   [illegible];
XX
DR   WPI; 2000-[illegible]/2[illegible].
DR   N-PSDB; AAA[illegible].
XX
PT   Process for preparation of [illegible] human serum albumin [illegible]
PT   yeast biased [illegible]
XX
PS   Disclosure; [illegible]pp; Chinese.
XX
CC   The method relates to a method of recombinantly producing human serum
CC   albumin (HSA) in yeast by altering the coding sequence [illegible]
CC   [illegible] yeast [illegible]. The complete HSA gene (AAA[illegible]) was
CC   generated as three synthetic fragments (AAA10092-AA[illegible]) [illegible]
CC   recombinant DNA technology. Each HSA fragment was synthe[illegible]
CC   overlapping oligonucleotide fragments that were extended [illegible]
CC   represents the complete sequence of the HSA encoded by [illegible]
CC   with a yeast codon bias. The invention also covers a recombinant
CC   expression vector, yeast host [illegible] carrying the recombinant [illegible]
CC   vector and the process for producing human serum albumin [illegible]
CC   host cell, especially in secretory mode.
XX
SQ   Sequence   [illegible] AA;

  Query Match            [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity  [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVT[illegible]
Db          1 DAHKS[illegible]QYLQQCPFEDHVKLVNEVT[illegible]

Qy         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPN[illegible]
Db         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPN[illegible]

Qy        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECC[illegible]
Db        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECC[illegible]

Qy        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFP[illegible]
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Db        181 [illegible]

Qy        241 VHTE[illegible]ADDRADLAKY[illegible]ENQ[illegible]SSKLKE[illegible]LLEKSH[illegible]AEVEN[illegible]MPA [illegible]
Db        241 VHTE[illegible]ADDRADLAKY[illegible]ENQ[illegible] [illegible]

Qy        301 [illegible]
Db        301 [illegible]

Qy        361 [illegible]
Db        361 [illegible] 420

Qy        421 PTLVEVSRNLGKVGSK[illegible]
Db        421 PTLVEVSRNLGKVGSK[illegible] 480

Qy        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHAD[illegible]
Db        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHAD[illegible]

Qy        541 KE[illegible]LEAVM[illegible]AAFVEK[illegible] 585
Db        541 KE[illegible] 585
```

RESULT 5
ABB79006
ID ABB79006 standard; Protein; 585 AA.
XX
AC ABB79006;
XX
DT 01-AUG-2002 (first entry)
XX
DE Human mature albumin protein SEQ ID No.10.
XX
KW Human; growth hormone; hGH; albumin; human serum albumin; HSA;
KW albumin fusion protein; cytostatic; anorectic; immunosuppressive;
KW antidiabetic; antirheumatic; antiarthritic; psoriatic; cancer;
KW non-Hodgkin's lymphoma; obesity; transplant rejection; psoriasis;
KW type 1 diabetes mellitus; rheumatoid arthritis.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Domain	1..194
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FT	Domain	1..105
FT		/label= subdomain
FT	Disulfide-bond	53..62
FT	Disulfide-bond	75..91
FT	Disulfide-bond	90..101
FT	Region	106..119
FT		/note= "flexible inter subdomain linker region"
FT	Domain	120..194
FT		/label= subdomain
FT	Disulfide-bond	124..169
FT	Disulfide-bond	168..177
FT	Domain	195..387
FT		/label= 2
FT	Domain	195..291
FT		/label= subdomain
FT	Disulfide-bond	245..253
FT	Disulfide-bond	265..279
FT	Disulfide-bond	278..289
FT	Region	292..315
FT		/note= "flexible inter-subdomain linker region"
FT	Domain	316..387
FT		/label= subdomain
FT	Disulfide-bond	316..361
FT	Disulfide-bond	360..369
FT	Domain	388..585
FT		/label= 3
FT	Domain	388..[illegible]
FT		/label= subdomain
FT	Disulfide-bond	392..438
FT	Disulfide-bond	[illegible]
FT	Disulfide-bond	461..477
FT	Disulfide-bond	476..487
FT	Region	492..511
FT		/note= "flexible inter subdomain linker region"
FT	Domain	512..585
FT		/label= subdomain
FT	Disulfide-bond	[illegible]
FT	Disulfide-bond	558..567

XX
PN WO200177137-A1.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US11988.
XX
PR 12-APR-2000; 2000US-[illegible].
PR 28-APR-2000; 2000US-[illegible].
PR 21-DEC-2000; 2000US-256931P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Haseltine WA;
XX
DR WPI; 2001-611723/70.
DR N-PSDB; AAD47288.
XX
PT New albumin fusion proteins, useful for treating diseases [illegible]
PT such as cancer, comprise therapeutic protein fused [illegible]
XX
PS Claim 1; Fig 11; 41pp; English.
XX
CC The present invention describes an albumin fusion protein (I) [illegible]
CC a therapeutic protein: X and (a fragment or variant of) [illegible]
CC comprising a fully defined sequence in ABB79006 of 585 [illegible]
CC (where the fragment or variant has albumin or therapeutic [illegible]
CC activity). (I) can have cytostatic, anorectic, immunosuppressive [illegible]
CC antidiabetic, antirheumatic, antiarthritic and psoriatic [illegible]
CC Albumin fusion proteins are stabilised therapeutic proteins [illegible]
CC antibodies to C5, C242 and C080 useful for treating various [illegible]
CC and disorders such as non Hodgkin's lymphoma, cancer, [illegible]
CC transplant rejection, type 1 diabetes mellitus, rheumatoid [illegible]
CC and psoriasis. Fusing albumin to therapeutic proteins st[illegible]
CC therapeutic protein, extends the shelf life and retains [illegible]
CC in vitro biological activity. It also reduces the need [illegible]
CC protein solutions with large excesses of carrier proteins [illegible]
CC loss of therapeutic proteins due to factors such as [illegible]
CC container. The fusion proteins are easily dispensed with [illegible]
CC formulation requiring minimal post storage manipulation. [illegible]
CC therapeutic proteins to albumin confers stability [illegible]
CC solution. The present sequence represents the mature human [illegible]
CC protein which is used in the exemplification of the present [illegible]
XX
SQ Sequence 585 AA;

Query Match [illegible]; Score [illegible]; DB 22; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Qy          1 DAHKSEVAHRFKD[illegible]NEKA[illegible]
Db          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAK[illegible]

Qy         61 N[illegible]
Db         61 N[illegible]

Qy        121 [illegible]
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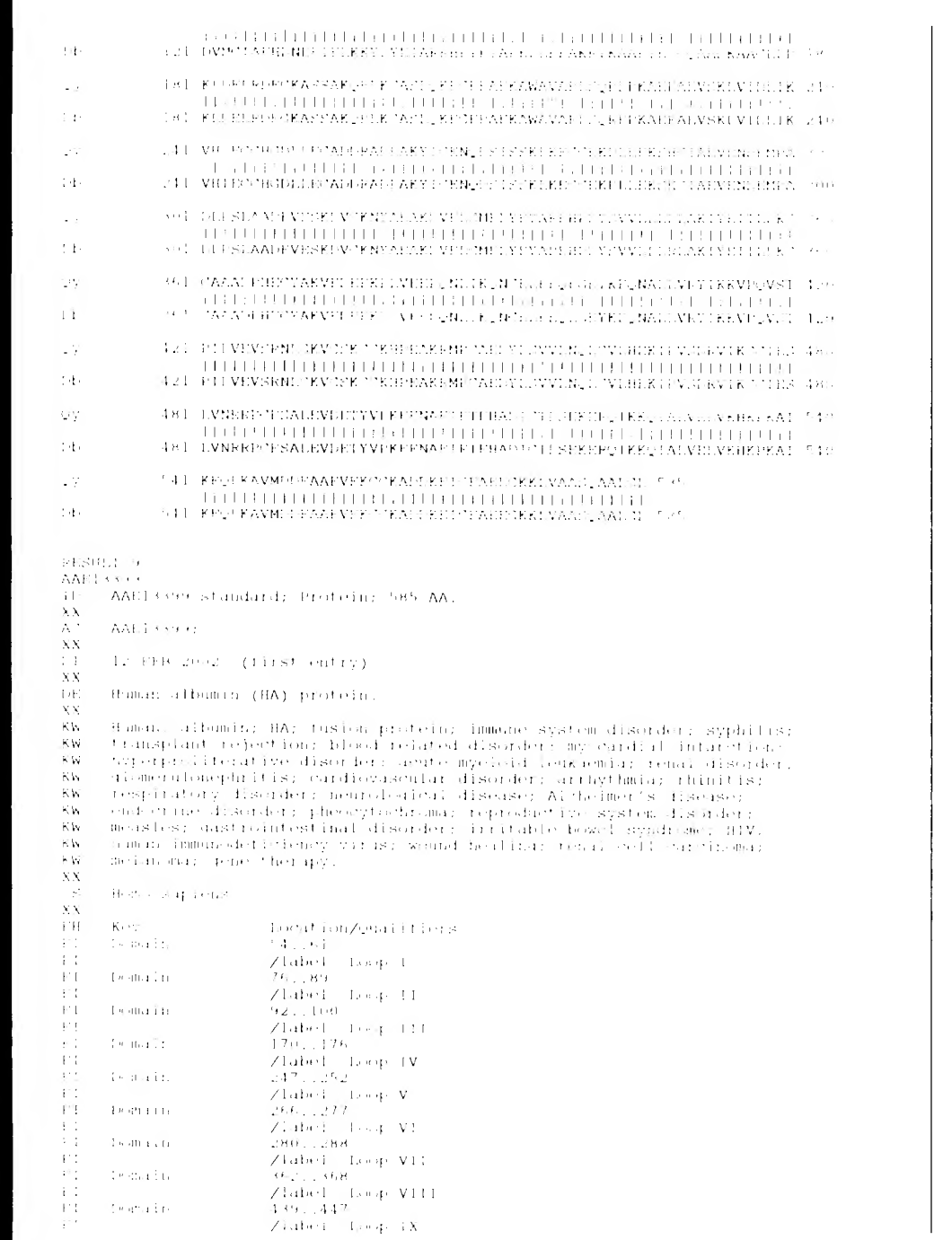

RESULT 9
AAE15490
ID AAE15490 standard; Protein; 585 AA.
XX
AC AAE15490;
XX
DT 12-FEB-2002 (first entry)
XX
DE Human albumin (HA) protein.
XX
KW Human; albumin; HA; fusion protein; immune system disorder; syphilis;
KW transplant rejection; blood related disorder; leukaemia; renal disorder;
KW hyperproliferative disorder; acute myeloid leukaemia; renal disorder;
KW glomerulonephritis; cardiovascular disorder; arrhythmia; rhinitis;
KW respiratory disorder; neurodegenerative disease; Alzheimer's disease;
KW endocrine disorder; pheochromocytoma; reproductive system disorder;
KW measles; gastrointestinal disorder; irritable bowel syndrome; HIV;
KW human immunodeficiency virus; wound healing; renal cell carcinoma;
KW melanoma; gene therapy.
XX
FH Key Location/Qualifiers
FT Domain 4..51
FT /label= Loop I
FT Domain 76..89
FT /label= Loop II
FT Domain 92..100
FT /label= Loop III
FT Domain 170..176
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FT Domain 247..252
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FT Domain 362..368
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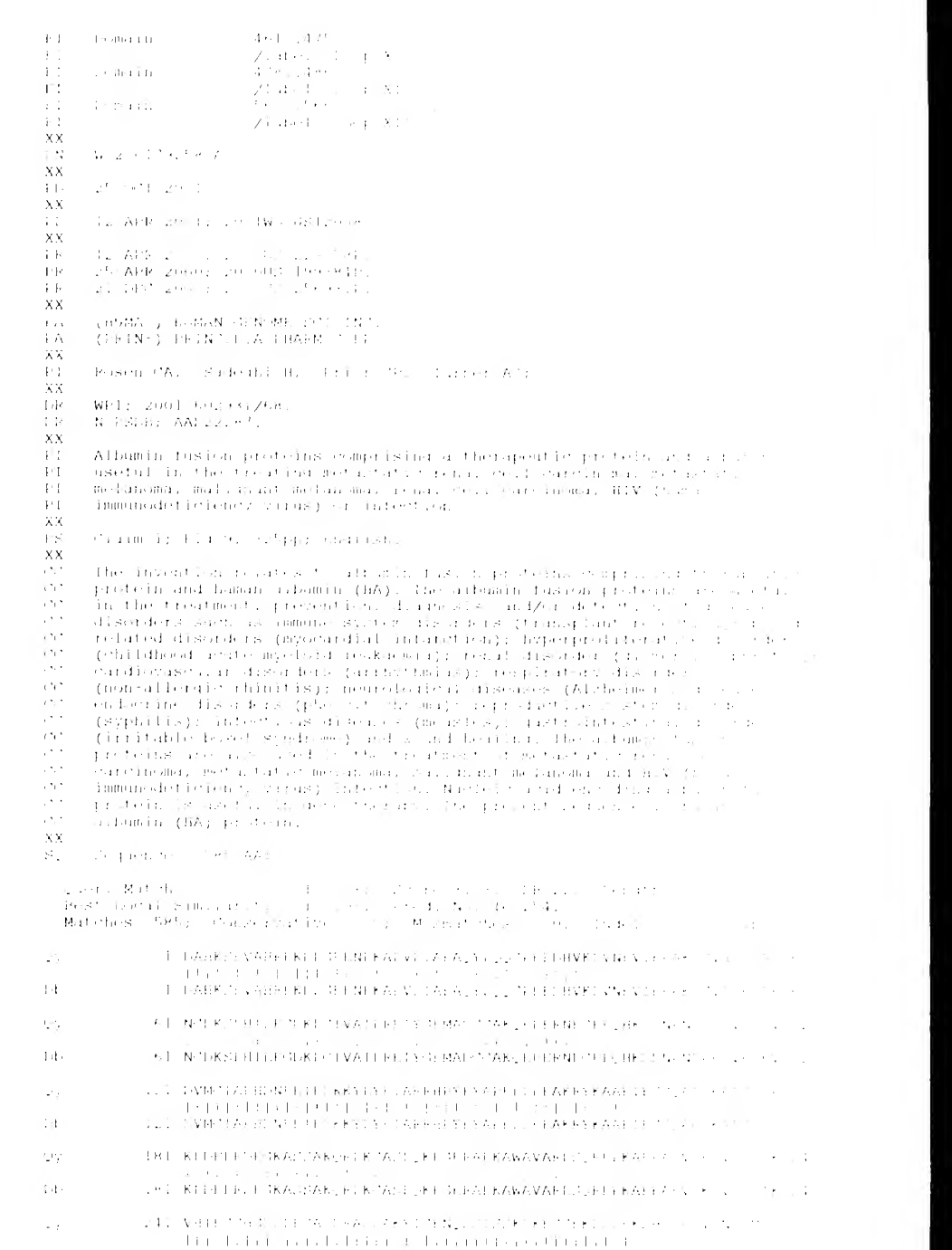
FT /label= Loop IX



RESULT 1
AAM52567
ID AAM52567 standard; Protein; 585 AA.
XX
AC AAM52567;
XX
DT 05-FEB-2002 (first entry)
XX
DE Mature human serum albumin.
XX
KW Human; serum albumin; HA; antiinflammatory; immunosuppressive; cardiant;
KW neuroprotective; neuroprotective; gene therapy; immune disorder; wound healing;
KW hyperproliferative disorder; renal disorder; cardiovascular disorder;
KW respiratory disorder; neurological disease; endocrine disorder;
KW reproductive system disorder; infectious disease;
KW gastrointestinal disorder.
XX
OS Homo sapiens.
XX
PN WO200179444-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US012013.
XX
PR 12-APR-2000; 2000US-197484P.
PR 25-APR-2000; 2000US-199484P.
PR 21-DEC-2000; 2000US-256961P.
XX
PA (HUMA) HUMAN GENOME SCI INC
XX
PI Rosen CA, Haseltine WA;
XX
DR WPI; 2001-616755/71.
DR N-PSDB; AAA04057.
XX
PT Albumin fusion proteins comprising a therapeutic protein and albumin,
PT useful in the treating immune system disorders (e.g. transplant
PT rejection), blood related disorders (e.g. myocardial infarction) and
PT hyperproliferative disorders.
XX
PS Claim 1; Fig 15; 606pp; English.
XX
CC The present invention relates to albumin fusion proteins, which comprise
CC a therapeutic protein and albumin. The present sequence is the protein
CC sequence for mature human serum albumin (HA), which was used to generate
CC the fusion proteins of the present invention. The albumin fusion proteins
CC are useful in the treatment, prevention, diagnosis, and/or detection of
CC diseases/disorders such as immune system disorders (e.g. transplant
CC rejection), blood related disorders (e.g. myocardial infarction),
CC hyperproliferative disorders (e.g. childhood acute myeloid
CC renal disorders (e.g. glomerulonephritis), cardiovascular
CC arrhythmia), respiratory disorders (e.g. non allergic thi
CC neurological disease (e.g. Alzheimer's disease), end
CC (e.g. pheochromocytoma), reproductive system disorders (e.g.
CC infectious diseases (e.g. measles), gastrointestinal disorders
CC irritable bowel syndrome) and cancer cachexia.
XX
SQ Sequence 585 AA;

Query Match Score ; DB 22:
Best Local Similarity ; Pred. No. 1e-254;
Matches ; Conservative ; Mismatches ; Indels ;

RESULT 11
AAE15129
ID AAE15129 standard; Protein; 585 AA.
XX
AC AAE15129;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human albumin (HA).
XX
KW Human; serum albumin; HA; fusion protein; therapeutic protein;
KW immune system disorder; transplant rejection; blood related disorder;
KW myocardial infarction; hyperproliferative disorder; childhood acute myeloid
KW renal disorder; cardiovascular disorder; arrhythmia;
KW respiratory disorder; gene therapy; non allergic thi
KW neurological disease; Alzheimer's disease; reproductive system
KW endocrine disorder; pheochromocytoma; infectious disease;
KW measles; gastrointestinal disorder; irritable bowel syndrome;

KW wound healing; antiinflammatory; immunosuppressive; neuroprotective;
KW cardiant; cytostatic; antileukaemic; antirheumatic; antimicrobial;
KW renal disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT Domain 76..89
FT /label= loop II
FT Domain 92..100
FT /label= loop III
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FT /label= loop IV
FT Domain 247..262
FT /label= loop V
FT Domain 266..277
FT /label= loop VI
FT Domain 280..288
FT /label= loop VII
FT Domain 362..368
FT /label= loop VIII
FT Domain 439..447
FT /label= loop IX
FT Domain 461..479
FT /label= loop X
FT Domain 478..480
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FT Domain 560..566
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XX
PN WO200179411-A2.
XX
PD 25-OCT-2001.
XX
PF 13-APR-2001; 2001WO-US12024.
XX
PR 14-APR-2000; 2000US-0550580.
PR 27-APR-2000; 2000US-0560841P.
PR 21-SEP-2000; 2000US-0664815.
XX
PA (HUMA) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2001-616754/71.
DR N-PSDB; AAB42644.
XX
PT Albumin fusion proteins comprising a therapeutic protein and albumin,
PT useful in the treating immune system disorders (e.g. transplant
PT rejection), blood related disorders (e.g. myocardial infarction) and
PT hyperproliferative disorders.
XX
PS Claim 1; Fig 6; 880pp; English.
XX
CC The invention relates to albumin fusion proteins comprising therapeutic
CC protein and human albumin (HA). Therapeutic protein fused to albumin
CC have an extended shelf life. The albumin fusion proteins are useful in
CC the treatment, prevention, diagnosis and/or detection of diseases,
CC disorders such as immune system disorders (e.g. transplant rejection),
CC blood related disorders (e.g. myocardial infarction), hyperproliferative
CC disorders (e.g. childhood acute myeloid leukaemia), renal disorders
CC (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias)
CC respiratory disorders (e.g. non-allergic rhinitis), neurological
CC diseases (e.g. Alzheimer's disease), endocrine disorders (e.g.
CC pheochromocytoma), reproductive system disorders (e.g. syphilis),
CC infectious diseases (e.g. measles), gastrointestinal disorders (e.g.
CC irritable bowel syndrome) and wound healing. Nucleic acids encoding
CC albumin fusion protein is used in gene therapy. The present sequence
CC is human albumin (HA) protein.
XX
SQ Sequence 585 AA;

Query Match [illegible]
Best Local Similarity [illegible]
Matches [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

RESULT 12
AAE12413
ID AAE12413 standard; [illegible]
XX
AC AAE12413;
XX
DT [illegible]
XX
DE Human albumin (HA).
XX
KW Human; albumin; HA; immune system disorder; transplant rejection;
KW blood related disorder; myocardial infarction; [illegible]
KW hyperproliferative disorder; childhood acute myeloid leukaemia;
KW renal disorder; glomerulonephritis; cardiovascular disorder; arrhythmia;
KW respiratory disorder; non-allergic rhinitis; [illegible]
KW neurological disease; Alzheimer's disease; endocrine disorder;
KW pheochromocytoma; reproductive system disorder; syphilis;
KW infectious disease; measles; gastrointestinal disorder; irritable bowel syndrome;
KW wound healing; gene therapy; [illegible]
KW cytostatic; antileukaemic; [illegible]
KW [illegible]
XX
OS Homo sapiens.
XX
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FT /label= [illegible]

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FT   Domain          170..176
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XX
PN   WO200179480-A1.
XX
PD   25-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US11991.
XX
PR   12-APR-2000; 2000US-229358P.
PR   25-APR-2000; 2000US-199384P.
PR   21-DEC-2000; 2000US-256931P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Haseltine WA;
XX
DR   WPI; 2001-616756/71.
DR   N-PSDB; AAD20005.
XX
PT   Albumin fusion proteins comprising a therapeutic protein and albumin,
PT   useful in the treating metastatic renal cell carcinoma, metastatic
PT   melanoma, malignant melanoma, renal cell carcinoma, HIV (human
PT   immunodeficiency virus) or infection -
XX
PS   Claim 1; Fig 9; 394pp; English.
XX
CC   The invention relates to human albumin (HA) fusion proteins and their
CC   corresponding nucleic acid sequences. Therapeutic proteins fused to
CC   albumin or its fragments have an extended shelf life. The albumin
CC   fusion proteins are useful in the treatment, prevention, diagnosis
CC   and/or detection of diseases, disorders such as immune system
CC   disorders (e.g. transplant rejection), blood related disorders (e.g.
CC   myocardial infarction), hyperproliferative disorders (e.g. childhood
CC   acute myeloid leukaemia, metastatic renal cell carcinoma, metastatic
CC   melanoma, malignant melanoma, renal cell carcinoma), renal disorders
CC   (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias),
CC   respiratory disorders (e.g. non-allergic rhinitis), neurological
CC   diseases (e.g. Alzheimer's disease), endocrine disorders (e.g.
CC   pheochromocytoma), reproductive system disorders (e.g. syphilis),
CC   infectious diseases (e.g. measles), gastrointestinal disorders (e.g.
CC   irritable bowel syndrome), HIV (human immunodeficiency virus) infection
CC   and wound healing. Nucleic acids encoding albumin fusion protein is
CC   used in gene therapy. The present sequence is human albumin.
XX
SQ   Sequence   585 AA;

  Query Match             100.0%;  Score 3105;  DB 22;  Length 585;
  Best Local Similarity   100.0%;  Pred. No. 1e-254;
  Matches  585;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVA[illegible] 60

Qy         61 NC[illegible]KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPN[illegible] 120
Db         61 NC[illegible]KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPN[illegible] 120

Qy        121 [illegible]VMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAA[illegible] 180
Db        121 [illegible]VMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAA[illegible] 180

Qy        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSK[illegible] 240
Db        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSK[illegible] 240

Qy        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
Db        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300

Qy        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAK[illegible] 360
Db        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAK[illegible] 360

Qy        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV[illegible] 420
Db        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV[illegible] 420

Qy        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCC[illegible] 480
Db        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCC[illegible] 480

Qy        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
Db        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540

Qy        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
Db        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585


RESULT 1[illegible]
AAB[illegible]
ID   AAB[illegible] standard; [illegible] AA.
XX
AC   AAB[illegible];
XX
DT   [illegible]-NOV-200[illegible]  (first entry)
XX
DE   Human serum albumin (HSA).
XX
KW   Human; albumin; cancer; cell proliferation; drug screening; [illegible]
XX
OS   Homo sapiens.
XX
PN   US[illegible]-A1.
XX
PD   14-AUG-200[illegible].
XX
PF   [illegible]
XX
PR   [illegible]
XX
PA   (UYFL-) UNIV [illegible].
XX
PI   Sonnenschein [illegible] AM;
XX
DR   WPI; 2001-[illegible]/[illegible].
DR   N-PSDB; AAD[illegible].
XX
PT   Measuring human cell proliferation, useful in drug screening [illegible]
PT   determine the potential for inhibiting cancer cell proliferation [illegible]
PT   for evaluating biopsied tumors, comprises employing albumin [illegible]
PT   peptide
XX
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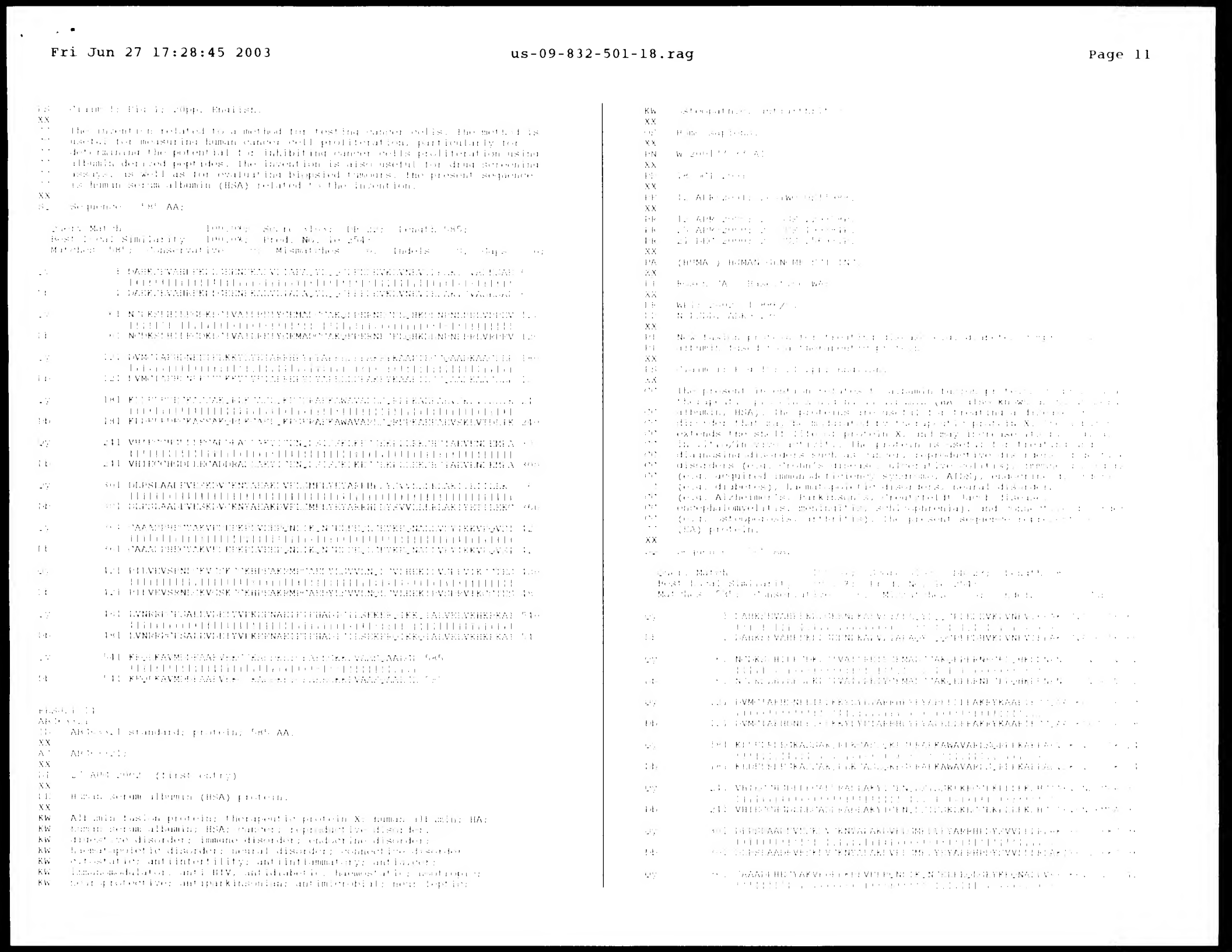

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Db        361 [illegible]AAADPHECYAKV[illegible]LVEEPQNLIKQN[illegible]KP[illegible] 420

Qy        421 FIILVEVSRNLGKVGSK[illegible]KHPEAKRMP[illegible]AEDYLSVVLNQL[illegible]VLHEKTPVSDRVTKCCTES 480
Db        421 FIIVEVSRNLGKVGSK[illegible]KHPEAKRMP[illegible]AED YLSVVLNQL[illegible]VLHEKTPVSDRVTKCCTES 480

Qy        481 LVNRR[illegible]FSALEVDETYVPKEFNAETFTFHA[illegible]ICTLSEKERQIKKQTALVELVKHKPKAT 540
Db        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540

Qy        541 KEQLKAVMDDFAAFVEK[illegible]KADDKETCFAEEGKKLVAASQAALGL 585
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RESULT 15
ABJ[illegible]

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AC   ABJ[illegible];
XX
DT   [illegible]-SEP-2002  (first entry)
XX
DE   B lymphocyte stimulator protein binding peptide related protein.
XX
KW   B lymphocyte stimulator protein binding protein; BLyS; immune disease;
KW   allergy; proliferative disease; infectious disease; arteriosclerosis;
KW   inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW   ischaemia; graft versus host disease; neurodegenerative disease;
KW   immunosuppressive; [illegible]; antirheumatic; antiarthritic;
KW   neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW   antiasthmatic; antiallergic; [illegible]; [illegible]; [illegible];
KW   dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW   antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS   Homo sapiens.
XX
PN   WO200216411-A2.
XX
PD   28-FEB-2002.
XX
PF   17-AUG-2001; 2001WO-US25856.
XX
PR   18-AUG-2000; 2000US-226700P.
XX
PA   (GEMA ) HUMAN GENOME SCI INC.
XX
PI   Beltzer JP,  Potter DM,  Fleming TL,  Rosen CA;
XX
DR   WPI; 2002-499775/53.
XX
PT   The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT   administering B lymphocyte stimulator binding polypeptide -
XX
PS   Disclosure; Page 379-382; 387pp; English.
XX
CC   The present invention relates to the treatment, prevention or
CC   amelioration of a disease or disorder associated with: aberrant B
CC   lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells
CC   of haematopoietic origin; or proliferative disease; and reducing,
CC   inhibiting or stimulating immunoglobulin production, B cell proliferation
CC   and graft rejection involving administration of BLyS binding polypeptide.
CC   The BLyS binding polypeptides are used in the treatment, prevention or
CC   amelioration of diseases such as immune system diseases, proliferative
CC   diseases, diseases of cells of hematopoietic origin, graft rejection,
CC   allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC   hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC   neurodegenerative diseases. The present sequence is a protein described
CC   in the invention.
XX
SQ   Sequence   585 AA;

  Query Match             100.0%;  Score [illegible];  DB 2[illegible];  Length 58[illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative    0;  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];

Qy          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVA[illegible]
Db          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVA[illegible]

Qy         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
Db         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120

Qy        121 DVM[illegible]
Db        121 DVM[illegible]

Qy        181 K[illegible]
Db        181 K[illegible]

Qy        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEV[illegible]
Db        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEV[illegible]

Qy        301 [illegible]AADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAK[illegible]
Db        301 [illegible]AADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAK[illegible]

Qy        361 [illegible]AAADPHECYAKV[illegible]
Db        361 [illegible]

Qy        421 [illegible]VLHEKTPVS[illegible]
Db        421 [illegible]KTPVS[illegible]

Qy        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
Db        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540

Qy        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
Db        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
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Search completed: June 27, 2003, [illegible]
Job time : 77 secs

OM protein - protein search, using sw model

Run on: June 27, 2003, 17:[illegible] ; Search time 44 Seconds
(without alignments)
[illegible] Million cell updates/sec

Title: US-09-832-501-18
Perfect score: 3103
Sequence: 1 DAHKSEVAHRFKDLGEENF..........[illegible]

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96[illegible] residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3103	100.0	609	1	ABHUS	serum albumin prec
2	2942	94.8	600	2	A47391	serum albumin prec
3	2620	84.4	608	2	S57632	serum albumin prec
4	2475.5	79.8	607	1	ABHOS	serum albumin prec
5	2446.5	78.8	607	1	ABBOS	serum albumin prec
6	2432.5	78.4	607	1	ABSHS	serum albumin prec
7	2427	78.2	608	1	ABRTS	serum albumin prec
8	2411.5	77.7	605	1	ABMSS	serum albumin prec
9	[illegible]	[illegible]	[illegible]	2	[illegible]	albumin - Mongolia
10	1861	60.0	453	2	A05139	serum albumin - he
11	1557.5	50.2	615	1	ABCHS	serum albumin prec
12	1253.5	40.4	609	2	[illegible]4258	alpha fetoprotein
13	1249.5	40.3	609	1	FPHU	alpha-fetoprotein
14	1242.5	40.0	609	1	FPGO	alpha-fetoprotein
15	1205	38.8	607	1	ABXL72	74K albumin precur
16	1161.5	38.[illegible]	265	2	I46986	albumin - dog (fra
17	1175.5	37.9	608	1	ABXL68	68K serum albumin
18	1084	34.9	605	1	FPMS	alpha fetoprotein
19	1067	34.4	611	1	FPRT	alpha fetoprotein
20	1055	34.0	599	1	A54906	afamin precursor -
21	928.5	29.9	611	2	S59517	serum albumin prec
22	928	29.9	608	2	A53195	afamin precursor -
23	747.5	24.1	608	1	ABONS1	serum albumin 1 pr
24	742.5	23.9	608	1	ABONS2	serum albumin 2 pr
25	699	22.5	382	2	A37253	serum albumin - fr
26	440.5	14.2	1423	1	S27941	serum albumin - se
27	386	12.4	474	1	VYHUD	vitamin D binding
28	385	12.4	476	1	VYRTD	Vitamin D binding
29	372	12.0	472	1	A35327	vitamin D binding
30	141	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
31	141	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
32	141.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
33	137.5	[illegible]	[illegible]	2	[illegible]	[illegible]
34	134.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
35	131	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
36	131	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
37	133.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
38	132.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
39	131	[illegible]	[illegible]	2	[illegible]	[illegible]
40	130	[illegible]	[illegible]	2	[illegible]	[illegible]
41	129	[illegible]	[illegible]	2	[illegible]	[illegible]
42	128.5	[illegible]	[illegible]	2	[illegible]	[illegible]
43	128	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
44	128	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
45	125.5	1.1	[illegible]	2	[illegible]	[illegible]

ALIGNMENTS

RESULT 1
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serum albumin precursor [validated] - human
N;Alternate names: [illegible]
N;Contains: kinetensin
C;Species: Homo sapiens (man)
C;Date: 29 Jul 1981 #sequence_revision [illegible] #text_change [illegible]
C;Accession: [illegible]
R;Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; [illegible]
Nucleic Acids Res. [illegible]
A;Title: The sequence of human serum albumin cDNA and [illegible]
A;Reference number: [illegible]
A;Accession: [illegible]
A;Molecule type: mRNA
A;Residues: [illegible]
A;Cross-references: EMBL:[illegible]
R;Dugaiczyk, A.; Law, S.W.; Dennison, O.E.
Proc. Natl. Acad. Sci. U.S.A. [illegible]
A;Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA
A;Reference number: [illegible]
A;Accession: [illegible]
A;Molecule type: mRNA
A;Residues: [illegible]
A;Cross-references: EMBL:[illegible]
R;Urano, Y.; Watanabe, K.; Sakai, M.; Tamaoki, T.
J. Biol. Chem. [illegible]
A;Title: The human albumin gene. Characterization of the [illegible]
A;Reference number: [illegible]
A;Accession: [illegible]
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: [illegible]
A;Cross-references: [illegible]
R;Watkins, S.; Madison, J.; [illegible]
Proc. Natl. Acad. Sci. U.S.A. [illegible]
A;Title: A nucleotide insertion and frameshift cause [illegible]
A;Reference number: [illegible]
A;Accession: I59290
A;Status: translated from [illegible]
A;Molecule type: DNA
A;Residues: 282-[illegible]
A;Cross-references: [illegible]
A;Note: this frameshift variant, [illegible]
R;Madison, J.; Galliano, M.; Watkins, S.; [illegible]
Proc. Natl. Acad. Sci. U.S.A. [illegible]
A;Title: Genetic variants of human serum albumin in Italy: [illegible]
A;Reference number: [illegible]
A;Accession: I59[illegible]
A;Status: translated from [illegible]
A;Molecule type: DNA
A;Residues: [illegible]
A;Cross-references: [illegible]

A;Note: this frame shift variant is designated albumin Bazzano, four additional variant
R;Monaya, J.; Parrilla, R.; Ayuso, M.S.
submitted to the EMBL Data Library, March 1995
A;Reference number: G38292
A;Accession: G01747
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-120,'G',122-455 <MEN>
A;Cross-references: EMBL:U22961; NID:g763428; PIDN:AAA64922.1; PID:g763431
R;Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
Biochem. J. 308, 321-325, 1995
A;Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast Kex2
A;Reference number: S55314; MUID:95277251; PMID:7755581
A;Accession: S55314
A;Molecule type: protein
A;Residues: 19-27 <LED>
R;Meloun, B.; Moravek, L.; Kostka, V.
FEBS Lett. 58, 134-137, 1975
A;Title: Complete amino acid sequence of human serum albumin.
A;Reference number: A91420; MUID:76187907; PMID:1225573
A;Accession: A91420
A;Molecule type: protein
A;Residues: 25-117,'EQ',120-154,'Q',156-193,'E',195-267,'H',269-299,'Y',302-355,'A',357
R;Roehr, U.; Spiteller, G.; Tripier, D.
Justus Liebigs Ann. Chem. 9, 881-884, 1988
A;Title: Isolation and structure elucidation of middle-molecular weight peptides from ur
A;Reference number: S06422
A;Note: this paper is in German, with an English abstract
A;Accession: S06422
A;Molecule type: protein
A;Residues: 25-48 <RUE>
R;Finch, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
Arch. Biochem. Biophys. 305, 595-599, 1993
A;Title: Mass spectrometric identification of modifications to human serum albumin treat
A;Reference number: S36882; MUID:93384321; PMID:8373198
A;Accession: S36882
A;Molecule type: protein
A;Residues: 45-67;141-160;311-337;469-490;572-581 <FIN>
R;Kausler, E.; Spiteller, G.
Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
A;Title: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin [illegible] der Hattermed
A;Reference number: S17599; MUID:92126241; PMID:1772596
A;Accession: S17599
A;Molecule type: protein
A;Residues: 25-54;354-357;431-447 <KAU>
A;Note: 49-Leu was also found
R;Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A;Title: Structures of histamine-releasing peptides formed by the action of acid proteas
A;Reference number: A45800; MUID:89341466; PMID:2474605
A;Accession: A45800
A;Molecule type: protein
A;Residues: 166-173 <CAR>
R;Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; Wa
Biochem. Biophys. Res. Commun. 136, 983-988, 1986
A;Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin tre
A;Reference number: A03239; MUID:86212189; PMID:3087352
A;Accession: A03239
A;Molecule type: protein
A;Residues: 166-173,'L' <MOG>
R;Galliano, M.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, S
Proc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
A;Title: Mutations in genetic variants of human serum albumin found in Italy.
A;Reference number: A38255; MUID:91062352; PMID:2247440
A;Accession: C38255
A;Molecule type: protein
A;Residues: 76-111 <GAL1>
A;Accession: B38255
A;Molecule type: protein
A;Residues: 82-105,'K',107-110 <GAL2>
A;Note: this variant is designated albumin Vibo Valentia
A;Accession: A38255
A;Molecule type: protein
A;Residues: 76-83,'K',85-100 <GAL>
A;Note: this variant is designated albumin Torino
R;Minchiotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. J. Biochem. 214, 437-444, 1993
A;Title: The structural characterization and bilirubin binding [illegible]
A;Reference number: S32298; MUID:93292[illegible]; PMID:8513793
A;Accession: S32298
A;Molecule type: protein
A;Residues: 255-263,'E',265-[illegible] <MIN>
A;Note: this variant is designated albumin Herborn
R;Minchiotti, L.; Galliano, M.; Stoppini, M.; Ferri, G.; Crespeau, [illegible]
Biochim. Biophys. Acta 1119, 232-238, 1992
A;Title: Two alloalbumins with identical electrophoretic mobility [illegible]
A;Reference number: S21078; MUID:92190239; PMID:1547703
A;Accession: S21078
A;Molecule type: protein
A;Residues: [illegible],'K',[illegible] <MIN>
A;Note: this variant is designated albumin Sondrio; another variant [illegible]
R;He, X.M.; Carter, D.C.
Nature 358, 209-215, 1992
A;Title: Atomic structure and chemistry of human serum albumin.
A;Reference number: A[illegible]; MUID:92334427; PMID:1630489
A;Contents: annotation; X-ray crystallography, 2.8 angstroms
R;Brown, J.R.; Shockley, P.; Behrens, P.Q.
in The Chemistry and Physiology of the Human Plasma Proteins, Bi[illegible]
A;Reference number: A94442
A;Contents: annotation; three-dimensional structure and disulfide [illegible]
R;Saber, M.A.; [illegible], P.; [illegible], L.; Meloun, B.
Collect. Czech. Chem. Commun. 42, 564-579, 1977
A;Title: Disulfide bonds in human serum albumin.
A;Reference number: A[illegible]
A;Contents: annotation; disulfide bonds
R;Jacobsen, C.
Biochem. J. 171, 453-459, 1978
A;Title: Lysine residue 240 of human serum albumin is involved in [illegible]
A;Reference number: A90299; MUID:78186630; PMID:656055
A;Contents: annotation; bilirubin-binding site
R;Peters, T.; Reed, R.G.
in Albumin: Structure, Biosynthesis, Function, Peters, T. and S[illegible]
A;Title: Serum albumin: conformation and active sites.
A;Reference number: A[illegible]
A;Contents: annotation; binding sites
R;Harper, M.E.; Dugaiczyk, A.
Am. J. Hum. Genet. 35, 565-572, 1983
A;Title: Linkage of the evolutionarily related serum albumin and [illegible]
A;Reference number: A[illegible]; MUID:83279982; PMID:6192711
A;Contents: annotation; gene position
R;Walker, J.E.
FEBS Lett. [illegible]
A;Title: Lysine residue [illegible] of human serum albumin is modified [illegible]
A;Reference number: A[illegible]; MUID:[illegible]; PMID:[illegible]
A;Contents: annotation
A;Note: the nonenzymatic transfer of an acetyl group from aspirin [illegible]
R;Bohney, J.P.; Fonda, M.L.; Feldhoff, R.C.
FEBS Lett. 298, 266-268, 1992
A;Title: Identification of Lys(199) as the primary binding site [illegible]
A;Reference number: A[illegible]; MUID:[illegible]; PMID:1544460
A;Contents: annotation
A;Note: the nonenzymatic binding of pyridoxal phosphate to Lys[illegible]
atase activity
C;Comment: Serum albumin, a predominant protein in the plasma [illegible]
lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, [illegible]
C;Comment: A large number of variants of human serum albumin have [illegible]
C;Genetics:
A;Gene: GDB:ALB
A;Cross-references: GDB:[illegible]; MIM:[illegible]
A;Map position: 4q11-4q13
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; phosph[illegible]
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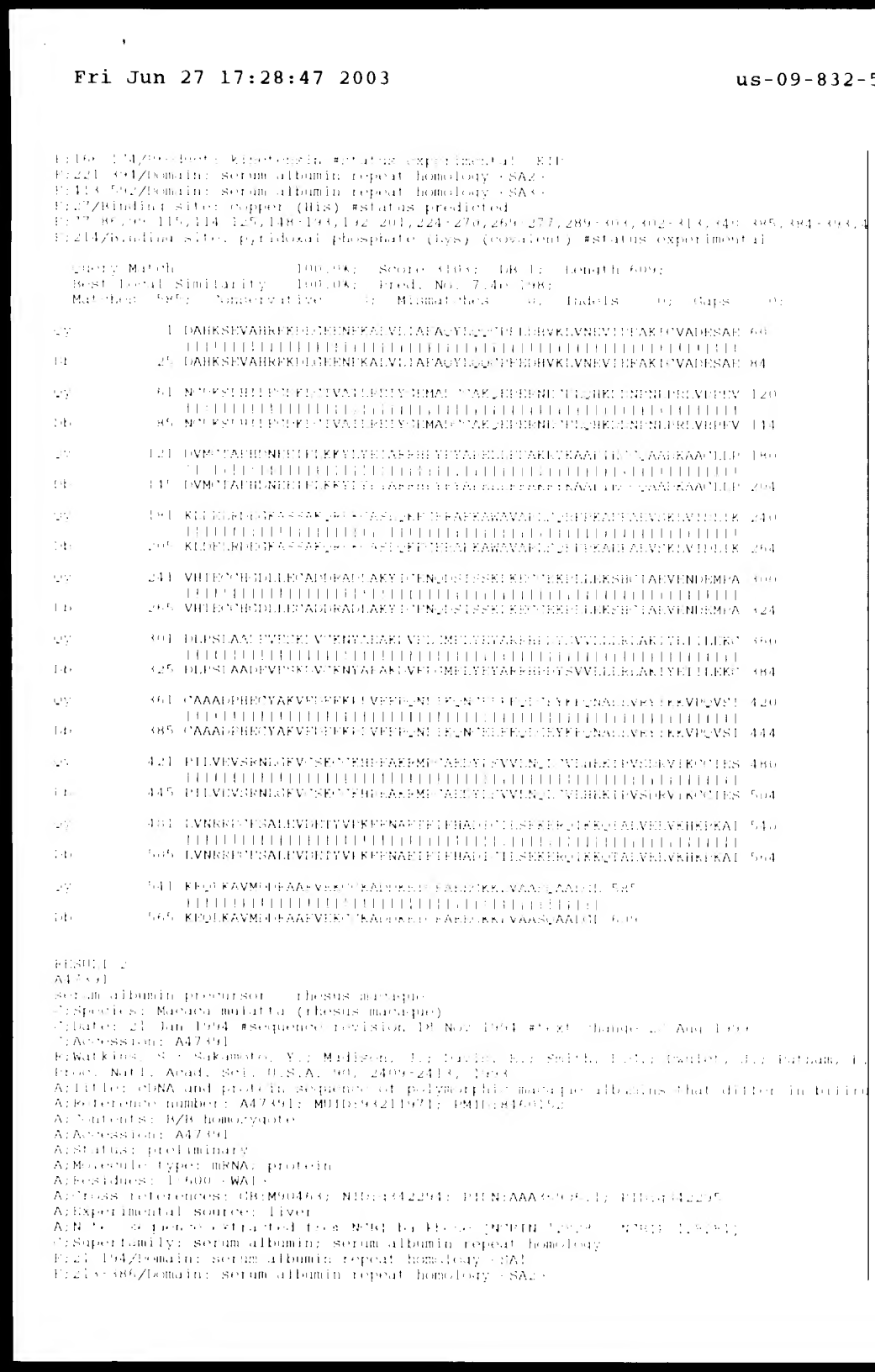
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-609/Product: serum albumin #status experimental <MAT>
F;29-202/Domain: serum albumin repeat homology <SA1>



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Query Match             84.4%;  Score 2620;  DB 2;  Length [illegible];
Best Local Similarity   82.0%;  Pred. No. 6.9e-166;
Matches  478;  Conservative   52;  Mismatches   53;  Indels    0;  Gaps    0;

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Db         25 EAHQSEIAHRFNDL[illegible]
Qy         61 [illegible]
Db         85 NCEKS[illegible]
Qy        [illegible]
Db        145 DAMCTAFHENE[illegible]
Qy        [illegible]
Db        [illegible]
Qy        241 VHIECCHGDLLECADDRADLAKY[illegible]
Db        [illegible]
Qy        [illegible]
Db        [illegible]
Qy        [illegible]
Db        [illegible]
Qy        421 PTLVEVSRNL[illegible]
Db        445 PTLVEVS[illegible]
Qy        481 LVNRR[illegible]
Db        [illegible] LVNKR[illegible]
Qy        [illegible]
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RESULT 4
ABBOS
serum albumin precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22 Jun 1999
C;Accession: S34053
R;Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, [illegible]
Eur. J. Biochem. 215, 205-212, 1993
A;Title: X ray and primary structure of horse serum albumin (Equus caballus) at [illegible] nm
A;Reference number: S34053; MUID:93345495; PMID:8344282
A;Accession: S34053
A;Molecule type: mRNA
A;Residues: 1-607 <HOA>
A;Cross-references: GB:X74045; NID:g[illegible]; PIDN:CAA52194.1; PID:g[illegible]
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, [illegible]
teroid hormones (weak bonds with these hormones promote their transfer across the membr[illegible]
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/[illegible] signal sequence #status predicted [illegible]
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-607/Product: serum albumin #status predicted <MAT>
F;[illegible]/Domain: serum albumin repeat homology <SA1>
F;[illegible]/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;[illegible]
F;[illegible]/Binding site: bilirubin (Lys) #status predicted

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Query Match             [illegible]
Best Local Similarity   [illegible];  Pred. No. [illegible];
Matches  415;  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible]

[illegible]
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RESULT [illegible]
ABBOS
serum albumin precursor [illegible] - bovine
N;Alternate names: [illegible] protein; preproalbumin
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision [illegible] #text_change [illegible]
C;Accession: [illegible]
R;Holowachuk, E.W.; Stoltenb[illegible]; Reed, R.G.; Peters Jr., T.
submitted to the EMBL Data Library, August [illegible]
A;Description: Bovine serum albumin: cDNA sequence and expression [illegible]
A;Reference number: [illegible]
A;Accession: [illegible]
A;Molecule type: mRNA
A;Residues: 1-607 <HOL>
A;Cross-references: EMBL:M[illegible]
R;Hirayama, K.; Akashi, S.; Furuya, M.; Fukuhara, K.
Biochem. Biophys. Res. Commun. [illegible]
A;Title: Rapid confirmation and revision of the primary structure [illegible]
A;Reference number: A[illegible]; MUID:[illegible]; PMID:[illegible]
A;Accession: A3640[illegible]
A;Molecule type: protein
A;Residues: 25-[illegible]
R;MacGillivray, R.T.A.; [illegible]
Eur. J. Biochem. [illegible], 477-[illegible], [illegible]
A;Title: Biosynthesis of bovine plasma proteins in a cell-free [illegible]
A;Reference number: A[illegible]; MUID:[illegible]; PMID:[illegible]
A;Accession: A[illegible]
A;Molecule type: protein

A;Residues: 1-[illegible] <MAG>
R;Hsieh, [illegible]; Lin, F.P.; Lam, M.[illegible]
Anal. Biochem. 170, 1-8, 1988
A;Title: Electroblotting onto glass fiber filter from an analytical isoelectric focusing [illegible]
A;Reference number: A60808; MUID:88267456; PMID:[illegible]
A;Accession: B60808
A;Molecule type: protein
A;Residues: 25-41 <HSI>
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu[illegible]
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10780
A;Molecule type: protein
A;Residues: 25-41,'H',43-57,59-64 <STR>
R;Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A;Title: Structures of histamine-releasing peptides formed by the action of acid proteas[illegible]
A;Reference number: A45800; MUID:89341406; PMID:2474609
A;Accession: D45800
A;Molecule type: protein
A;Residues: 163-172 <CAR>
R;Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
J. Biol. Chem. 262, 5968-5973, 1987
A;Title: Structure of a biologically active neurotensin-related peptide obtained from pe[illegible]
A;Reference number: A26693; MUID:87194895; PMID:[illegible]
A;Accession: A26693
A;Molecule type: protein
A;Residues: 165-172,'L' <CA2>
R;Reed, R.G.; Putnam, F.W.; Peters Jr., T.
Biochem. J. 191, 867-868, 1980
A;Title: Sequence of residues 400-403 of bovine serum albumin.
A;Reference number: A90309; MUID:82023364; PMID:7283978
A;Accession: A90309
A;Molecule type: protein
A;Residues: 402-433 <REE>
R;Brown, J.R.
Fed. Proc. 34, 591, 1975
A;Title: Structure of bovine serum albumin.
A;Reference number: A91458
A;Accession: A91458
A;Molecule type: protein
A;Residues: 25-41,'H',43-117,'EQ',120-179,181-189,'E',191-194,'A',196-213,'T',215-288,'[illegible]
R;Brown, J.R.
Submitted to the Atlas, April 1975
A;Reference number: A94551
A;Accession: A94551
A;Molecule type: protein
A;Residues: 190-195 <BR2>
R;Brown, J.R.
Fed. Proc. 33, 1389, 1974
A;Reference number: A91457
A;Contents: annotation; disulfide bonds
R;Werlen, R.C.; Offord, R.E.; Rose, K.
Biochem. J. 302, 907-911, 1994
A;Title: Preparation and characterization of novel substrates of insulin proteinase (E[illegible]
A;Reference number: S55232; MUID:95031935; PMID:7945219
A;Accession: S55232
A;Status: preliminary
A;Molecule type: protein
A;Residues: 529-536;569-572 <WER>
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; copper binding; duplication; plasma
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-607/Product: serum albumin #status experimental <MAT>
F;25-211/Domain: serum albumin repeat homology <SA1>
F;220-403/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;77-86,99-115,114-125,147-192,191-200,223-269,268-276,[illegible]

Query Match 78.8%; Score 2148.5; DB 1; Length 607;

Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 447; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy 1 DAHK[illegible]VAHRFKD[illegible]ENFKALV[illegible]IAFA[illegible]Y[illegible]HVK[illegible]VNEV[illegible]
Db 25 [illegible]THK[illegible]EIAHRFKD[illegible]KV[illegible]IAF[illegible]HVK[illegible]VN[illegible]

Qy 61 N[illegible]HTLF[illegible]DK[illegible]TVAT[illegible]ETYGEMA[illegible]AK[illegible]RNE[illegible]HK[illegible]
Db 85 G[illegible]EK[illegible]HTLFGDE[illegible]KVASLRETYG[illegible]MA[illegible]EK[illegible]RNE[illegible]HK[illegible]

Qy 121 [illegible]VM[illegible]TAF[illegible]KKYLYE[illegible]IARRHPYFYAPELLFFAKRYKAA[illegible]
Db 144 N[illegible]KA[illegible]KKFW[illegible]KYLYEIARRHPYFYAPELLYYANKYN[illegible]

Qy 181 KLDEL[illegible]KASSAK[illegible]K[illegible]A[illegible]KA[illegible]AKAWAVAR[illegible]PKA[illegible]
Db 204 K[illegible]KVLA[illegible]KA[illegible]AKAWSVAR[illegible]KA[illegible]

Qy 241 VH[illegible]
Db 264 VHKE[illegible]

Qy 301 [illegible]
Db 324 N[illegible]

Qy 361 CAAA[illegible]YAKV[illegible]
Db 384 CAK[illegible]

Qy 421 P[illegible]
Db 444 P[illegible]

Qy 481 LVNR[illegible]
Db 504 LVNR[illegible]

Qy 541 KE[illegible]LKAVM[illegible]AA[illegible]VEK[illegible]KK[illegible]VAAS[illegible]AAL[illegible]
Db 564 [illegible]LK[illegible]VMENFVA[illegible]KKLVV[illegible]

RESULT 6
ABSHS
serum albumin precursor [illegible]
C;Species: Ovis orientalis aries [illegible]
C;Date: [illegible]
C;Accession: S06[illegible]
R;Brown, W.M.; [illegible]
Nucleic Acids Res. 17, [illegible]
A;Title: Nucleotide and deduced [illegible]
A;Reference number: [illegible]
A;Accession: S06[illegible]
A;Molecule type: mRNA
A;Residues: 1-607 <BRO>
A;Cross-references: EMBL:X[illegible]; NID:[illegible]; PIDN:CAA[illegible]
C;Comment: Serum albumin is synthesized in the liver as [illegible]
teroid hormones (weak bonds with them [illegible]
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-607/Product: serum albumin #status predicted <MAT>
F;25-2[illegible]/Domain: serum albumin repeat homology <SA1>
F;22[illegible]/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;77-86,99-115,114-125,147-[illegible]
F;26[illegible]/Binding site: bilirubin (Lys) #status predicted

Query Match [illegible]; Score [illegible]; DB 1; Length [illegible];

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  Best Local Similarity   75.0%;  Pred. No. 1.8e-153;
  Matches  437;  Conservative   7[illegible];  Mismatches   72;  Indels   [illegible];  Gaps   [illegible];

Qy          1 DAHK[illegible] 60
Db         25 DTHKS[illegible] 84

Qy         61 [illegible] 120
Db         85 [illegible]

Qy        121 DVM[illegible]
Db        144 DTLCAE[illegible]

Qy        181 [illegible]
Db        204 [illegible]

Qy        241 VH[illegible]
Db        264 VHE[illegible]

Qy        301 DLPS[illegible]
Db        324 [illegible]

Qy        361 CAAA[illegible] 420
Db        384 CAEE[illegible]

Qy        421 PLVE[illegible]
Db        444 PLVE[illegible]

Qy        481 LVNRR[illegible]
Db        504 LVNKK[illegible]

Qy        541 KE[illegible]
Db        564 DEQLKTVMENFVAFVDK[illegible] 606
```

RESULT 7
ABRTS
serum albumin precursor - rat
N;Alternate names: preproalbumin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-May-1979 #sequence_revision 31 May-1979 #text_change 22 Jun-1999
C;Accession: A93872; A92211; A91946; A91940; [illegible]; I57621; A[illegible]
R;Sargent, T.D.; Yang, M.; Bonner, J.
Proc. Natl. Acad. Sci. U.S.A. 78, 243-246, 1981
A;Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
A;Reference number: A93872; MUID:81220722; PMID:[illegible]
A;Accession: A93872
A;Molecule type: mRNA
A;Residues: 1-608 <SAR>
A;Cross-references: GB:V01222; [illegible]
R;Strauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
J. Biol. Chem. 252, 6846-6855, 1977
A;Title: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analys
A;Reference number: A92211; MUID:77249657; PMID:[illegible]
A;Note: cleavages during protein maturation
A;Accession: A92211
A;Molecule type: protein
A;Residues: 1-39 [illegible]
R;Isemura, S.; Ikenaka, T.
J. Biochem. 83, 35-48, 1978
A;Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleava
A;Reference number: A91946; MUID:78129429; PMID:[illegible]
A;Accession: A91946
A;Molecule type: protein
A;Residues: 25-[illegible]
R;Isemura, S.; Ikenaka, T.
J. Biochem. 7[illegible]
A;Title: Fragmentation of rat serum albumin by cyanogen bromide [illegible]
A;Reference number: A91940; MUID:[illegible]; PMID:[illegible]
A;Accession: A91940
A;Molecule type: protein
A;Residues: [illegible]
A;Note: 262 Leu was also found
R;[illegible]
Cancer Res. [illegible]
A;Title: [illegible] alpha-fetoprotein.
A;Reference number: A90758; [illegible]
A;Contents: annotation; copper binding
R;Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.R.
[illegible]
A;Title: Structures of histamine-releasing peptides formed by [illegible]
A;Reference number: [illegible]; PMID:2474609
A;Accession: [illegible]
A;Status: preliminary
A;Molecule type: protein
A;Residues: [illegible]
R;Heard, J.
[illegible] 1987
A;Title: Determinants of rat albumin promoter tissue specificity [illegible]
A;Reference number: [illegible] 47556
A;Accession: I57621
A;Status: [illegible]
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: GB:M[illegible]; NID:[illegible]; PIDN:AAA40712.1; [illegible]
C;Superfamily: serum albumin; [illegible] repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-608/[illegible] serum albumin [illegible] experimental <MAT>
F;29-202/Domain: serum albumin repeat homology <SA1>
F;22[illegible]/Domain: serum albumin repeat homology <SA2>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;2[illegible]/Binding site: copper (His) #status experimental
F;77-86,99-115,114-125,148-[illegible],192-201,224-270,269-277,289-[illegible]

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  Query Match            [illegible]%;  Score 242[illegible];  DB 1;  Length [illegible];
  Best Local Similarity   73.4%;  Pred. No. 1.7e-153;
  Matches  428;  Conservative   [illegible];  Mismatches   7[illegible];  Indels   [illegible];  Gaps   [illegible];

Qy          1 DAHKSEVAHRFKD[illegible]NFKALVLIAFAQYL[illegible]VKLVNEVTEFAK[illegible]
Db         25 EAHKSEIAHRFKDLGEQHFKGLVLIAFSQYLQK[illegible]KLVQEVTDFAKTCVADENA[illegible] 84

Qy         61 [illegible]
Db         85 [illegible]

Qy        121 [illegible]
Db        145 [illegible]

Qy        181 [illegible]
Db        205 [illegible]

Qy        241 VHTE[illegible]
Db        265 [illegible]

Qy        301 [illegible]
Db        325 [illegible]

Qy        361 [illegible]
Db        385 [illegible]
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[illegible]

RESULT 8
ABPGS
serum albumin precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31 Dec 1993 #sequence_revision 31 Dec 1993 #text_change [illegible]
C;Accession: S01382; A61006
R;Weinstock, J.; Baldwin, G.S.
Nucleic Acids Res. 16, 9045, 1988
A;Title: Nucleotide sequence of porcine liver albumin.
A;Reference number: S01382; MUID:89016582; PMID:[illegible]
A;Accession: S01382
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-605 <WEI>
A;Cross-references: EMBL:X12422; NID:g1875; PIDN:CAA30[illegible]; PID:g833798
R;Limeback, H.; Sakarya, H.; Chu, W.; Mackinnon, M.
J. Bone Miner. Res. 4, 235-241, 1989
A;Title: Serum albumin and its acid hydrolysis peptides dominate preparations of mineral
A;Reference number: A61006; MUID:89269769; PMID:272892[illegible]
A;Accession: A61006
A;Molecule type: protein
A;Residues: 23-51,'X',53-54,'XXXGY',146,'E',148,'E',150-151,'XVN',155-[illegible] <LIM>
A;Experimental source: dental enamel
A;Note: albumin and other serum proteins are also found in bone
C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper,
[illegible]id hormones (weak bonds with these hormones promote their transfer across the membra
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F;17-22/Domain: propeptide #status predicted <PRO>
F;23-605/Product: serum albumin #status predicted <MAT>
F;27-[illegible]/Domain: serum albumin repeat homology <SA1>
F;[illegible]/Domain: serum albumin repeat homology <SA2>
F;[illegible]/Domain: serum albumin repeat homology <SA3>
F;[illegible],84,97-113,112-123,145-[illegible],198,221-267,266-274,[illegible]
F;[illegible]/Binding site: bilirubin (Lys) #status predicted

Query Match [illegible]; Score 2411.5; DB 1; Length 605;
Best Local Similarity 76.0%; Pred. No. 4.3e-152;
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

RESULT 9
[illegible]
albumin - [illegible]
C;Species: [illegible]
C;Date: [illegible]
C;Accession: [illegible]
[illegible]
DNA Res. 4, [illegible]
A;Title: Sequencing [illegible]
A;Reference number: [illegible]
A;Accession: [illegible]
A;Molecule type: mRNA
A;Residues: 1-609 [illegible]
A;Cross-references: [illegible]
A;Experimental source: liver
C;Superfamily: serum albumin; serum albumin repeat homology
F;[illegible]/Domain: serum albumin repeat homology <SA2>

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

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Qy        422 [illegible] 481
Db        447 [illegible]

Qy        482 VNKRP[illegible] 541
Db        507 VNKRP[illegible] 566

Qy        542 EQLKAVMDDFAAFVEK[illegible] 
Db        567 EQLKKVM[illegible]
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RESULT 16
A05139
serum albumin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1987 #sequence_revision 17 Mar 2000 #text_change 17 Mar 20[illegible]
C;Accession: A05139; I48638
R;Minghetti, P.P.; Law, S.W.; Dugaiczyk, A.
Mol. Biol. Evol. 2, 347-358, 1985
A;Title: The rate of molecular evolution of alpha-fetoprotein approaches that of pseudog
A;Reference number: A93055; MUID:88216123; PMID:2452956
A;Accession: A05139
A;Molecule type: mRNA
A;Residues: 1-418 <MIN>
A;Cross-references: GB:M16111; NID:g191764; PIDN:AAA[illegible]
R;[illegible], C.; Deschatrette, J.; Meunier Rotival, M.
Gene 88, 181-186, 1990
A;Title: Empty and occupied insertion site of the truncated LINE 1 repeat located in the
A;Reference number: I48638; MUID:90269606; PMID:1971802
A;Accession: I48638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 379-453 <BOC>
A;Cross-references: EMBL:X[illegible]; NID:g52[illegible]; PIDN:CAA[illegible]; PID:g[illegible]
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-104/Domain: serum albumin repeat homology (fragment) <SA1>
F;123-296/Domain: serum albumin repeat homology <SA2>
F;315-453/Domain: serum albumin repeat homology (fragment) <SA3>

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  Query Match             60.0%;  Score 1861;  DB 2;  Length 45[illegible];
  Best Local Similarity   72.2%;  Pred. No. 8.[illegible]e-116;
  Matches  327;  Conservative   [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy         75 [illegible] 134
Db          1 [illegible]

Qy        135 [illegible] 194
Db         61 [illegible] 120

Qy        195 [illegible] 254
Db        121 [illegible] 180

Qy        255 [illegible] 314
Db        181 [illegible] 240

Qy        315 [illegible] 374
Db        241 [illegible] 300

Qy        375 [illegible] 434
Db        301 [illegible] 360

Qy        435 [illegible] 494
Db        361 [illegible] 420

Qy        495 [illegible] 527
Db        421 [illegible] 453
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RESULT 17
ABCHS
serum albumin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: [illegible]
C;Accession: S1[illegible]; A05078; A1[illegible]
R;Cassady, A.I.; Salkfid, C.K.; [illegible]; Wallace, [illegible]
submitted to the EMBL Data Library, July 19[illegible]
A;Reference number: S1[illegible]
A;Accession: S15571
A;Molecule type: mRNA
A;Residues: 1-615 <CAS>
A;Cross-references: EMBL:X[illegible]; NID:[illegible]; PIDN:CAA43098.1; PID:[illegible]
R;[illegible], R.J.G.; Wiskocil, R.; [illegible]
J. Biol. Chem. 258, 4556-4564, 1983
A;Title: The 5' noncoding and flanking regions of the avian [illegible]
A;Reference number: A05078; MUID:[illegible]; PMID:6187737
A;Accession: A05078
A;Molecule type: DNA
A;Residues: 1-[illegible] <HAC>
A;Cross-references: [illegible]
R;Rosen, A.M.; Geller, D.M.
Biochem. Biophys. Res. Commun. 78, 1060-1066, 1977
A;Title: Chicken microsomal albumin: amino terminal sequence [illegible]
A;Reference number: A1[illegible]; MUID:[illegible]; PMID:[illegible]
A;Accession: A1[illegible]
A;Molecule type: protein
A;Residues: [illegible]
C;Comment: Serum albumin is synthesized in the liver as preproalbumin [illegible]
[illegible] with these hormones promote their transfer across [illegible]
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-2[illegible]/Domain: propeptide #status predicted <PRO>
F;2[illegible]-6[illegible]/Product: serum albumin #status predicted <MAT>
F;32-206/Domain: serum albumin repeat homology <SA1>
F;2[illegible]-[illegible]/Domain: serum albumin repeat homology <SA2>
F;417-[illegible]/Domain: serum albumin repeat homology <SA3>
F;[illegible]/Binding site: copper (His) #status predicted
F;[illegible]

```
  Query Match             [illegible];  Score [illegible];  DB 1;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. 1.1e-[illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  192;  Indels  [illegible];  Gaps  [illegible];

Qy          3 [illegible]
Db         [illegible]

Qy         63 [illegible]
Db         [illegible]

Qy        123 [illegible]
Db        150 [illegible]

Qy        183 [illegible]
Db        210 [illegible]

Qy        243 [illegible]
Db        270 [illegible]

Qy        [illegible]
```

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Db        [illegible] 509
Qy        422 [illegible] 121
Db        [illegible] 449
Qy        422 ILVEVSRNLGKV[illegible] 481
Db        450 LLLEIGKEMI[illegible] 509
Qy        482 VNE[illegible]FNALLFT[illegible] 541
Db        510 ANP[illegible]FIAM[illegible] 569
Qy        542 EQLKAVM[illegible]FAAFVEK[illegible]KAL[illegible]FAL[illegible]KLVAA[illegible]AALGL 585
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RESULT 12
JC4258
alpha fetoprotein precursor - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 27-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 20-Aug-1999
C;Accession: JC4258
R;Nishio, H.; Gibbs, P.E.M.; Minghetti, P.P.; Zielinski, R.; Dugaiczyk, A.
Gene 162, 213-220, 1995
A;Title: The chimpanzee alpha-fetoprotein encoding gene shows structural similarity to t
A;Reference number: JC4258; MUID:96032345; PMID:7557431
A;Accession: JC4258
A;Molecule type: DNA
A;Residues: 1-609 <NIS>
A;Cross-references: GB:[illegible], NID:[illegible], PIDN:AAA[illegible], PID:[illegible]
C;Comment: This protein is a plasma protein produced in the fetal and neonatal liver and
 similar properties and structure.
C;Genetics:
A;Gene: afp
A;Map position: 4q
A;[illegible]
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-609/Product: alpha-fetoprotein #status predicted <MAT>
F;[illegible]/Domain: serum albumin repeat homology <SA1>
F;[illegible]/Domain: serum albumin repeat homology <SA2>
F;[illegible]/Domain: serum albumin repeat homology <SA3>
F;[illegible]/Binding site: carbohydrate (Asn) (covalent) #status predicted

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  Query Match             40.4%;  Score 1253.5;  DB 2;  Length 609;
  Best Local Similarity   45.1%;  Pred. No. 1.9e-75;
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Qy          3 HKSE      VAHRFKDLGEENFKALVLIAFAQ[illegible] 52
Db         22 HKNEYGIASILDSYQCTAEINLIDLATIFFAQFVQEATYKEVSKMVKDALTAIEKPTGDE 81
Qy         56 [illegible] 115
Db         82 [illegible] 1[illegible]
Qy        117 [illegible] 17[illegible]
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Qy        177 [illegible] 2[illegible]
Db        201 [illegible] 2[illegible]
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Qy        297 EMPADL[illegible] [illegible]
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Qy        4[illegible] [illegible]
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Db        441 [illegible]
Qy        477 [illegible]
Db        501 [illegible]
Qy        5[illegible] [illegible]
Db        561 [illegible]
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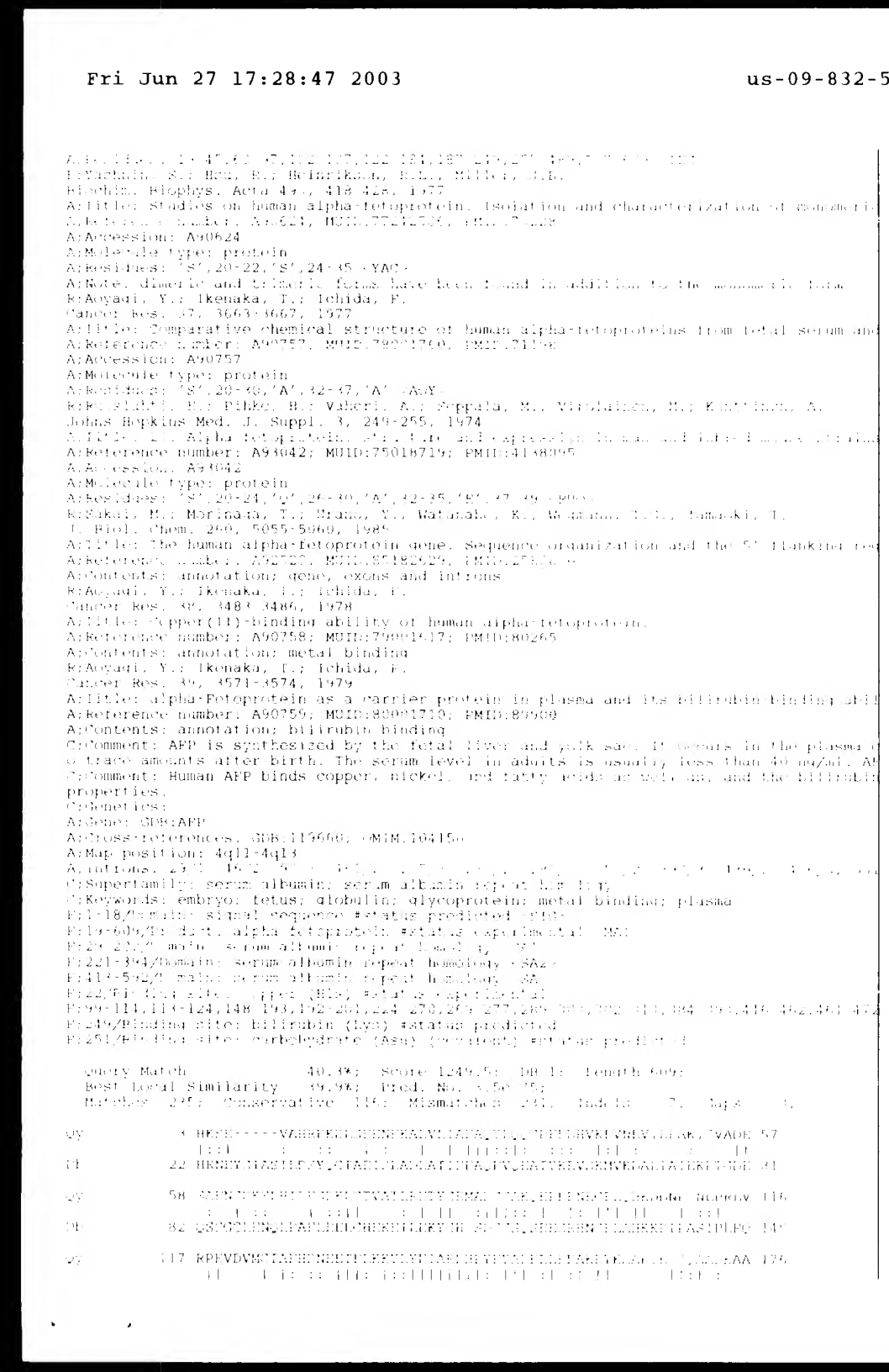
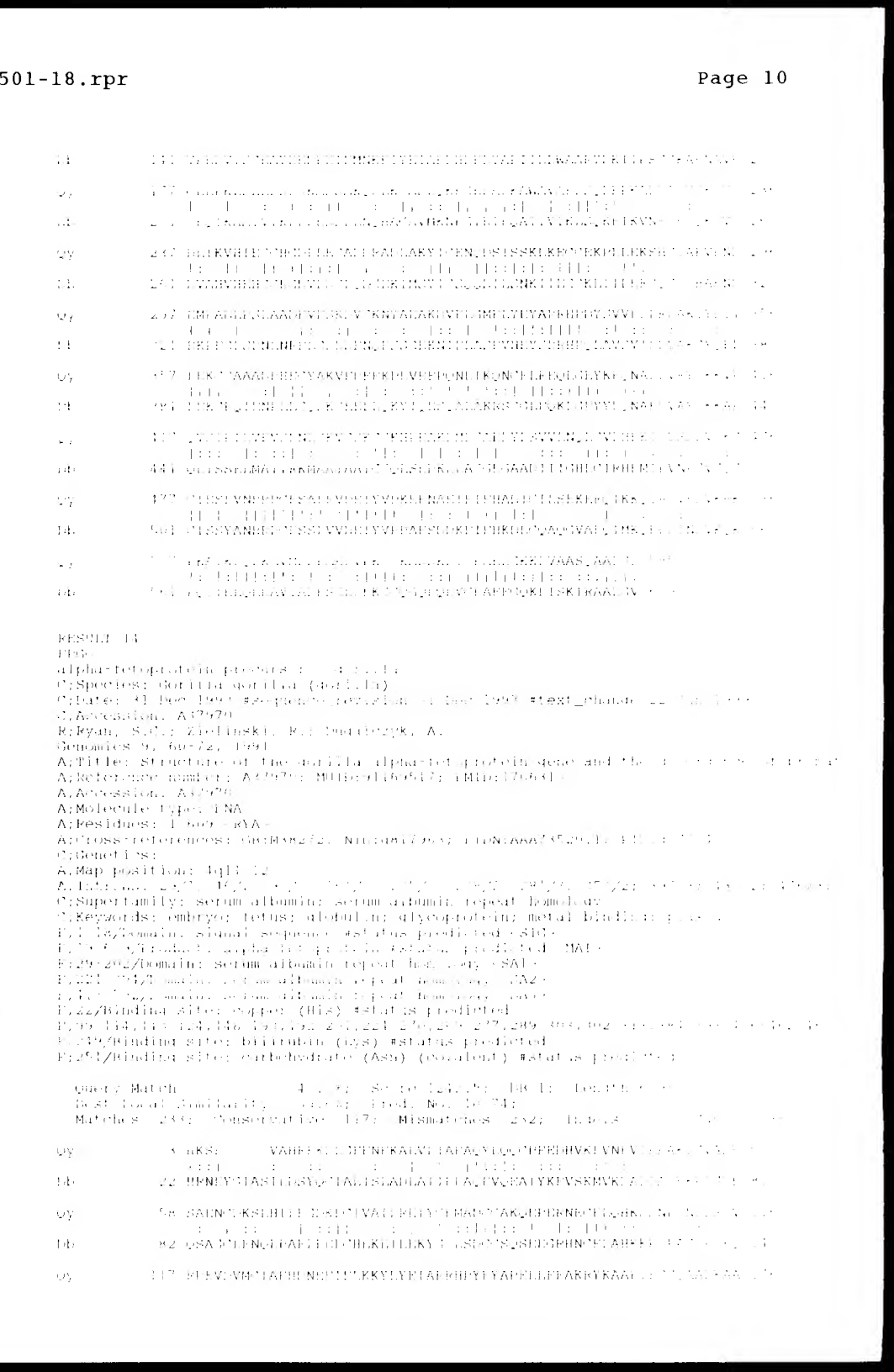
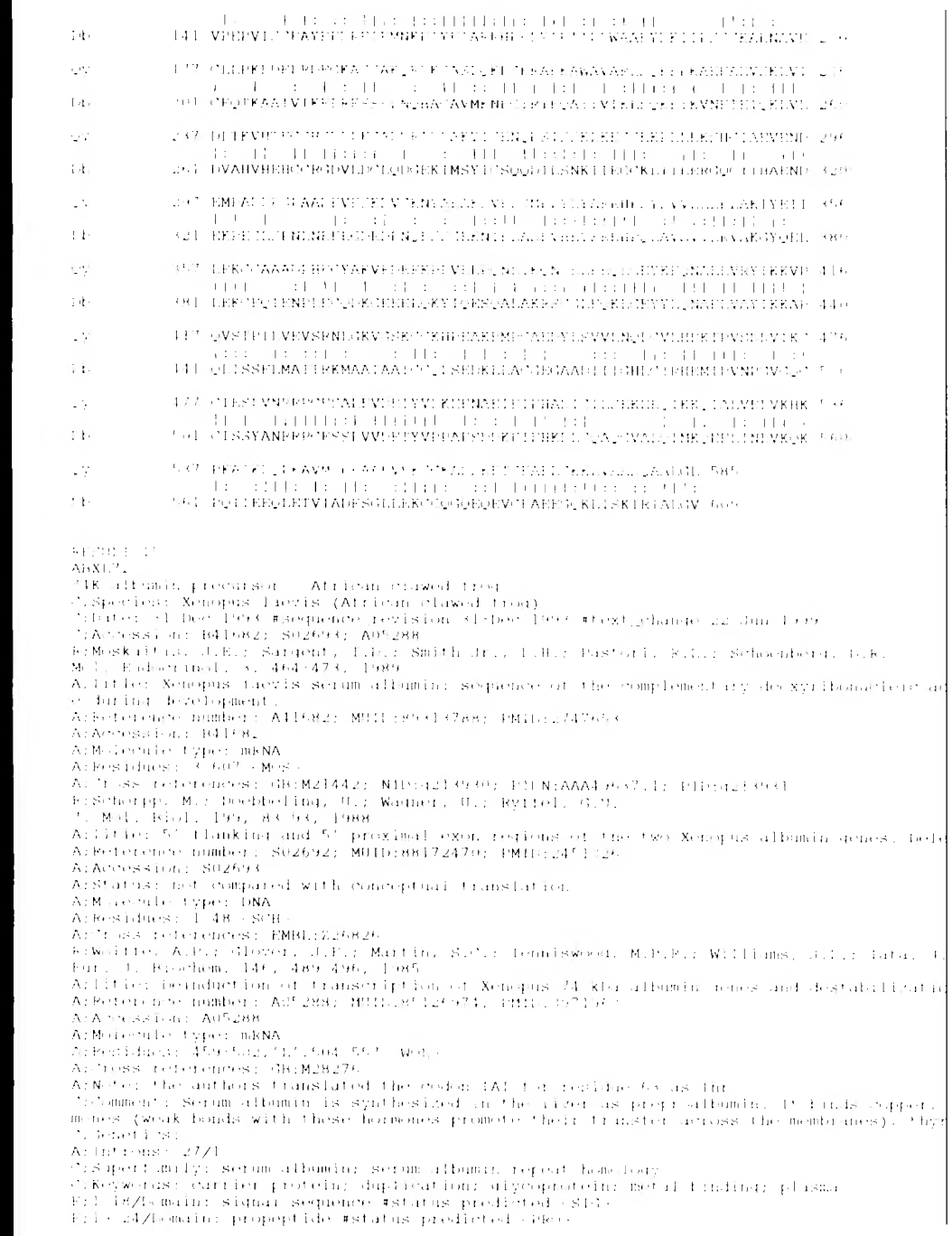
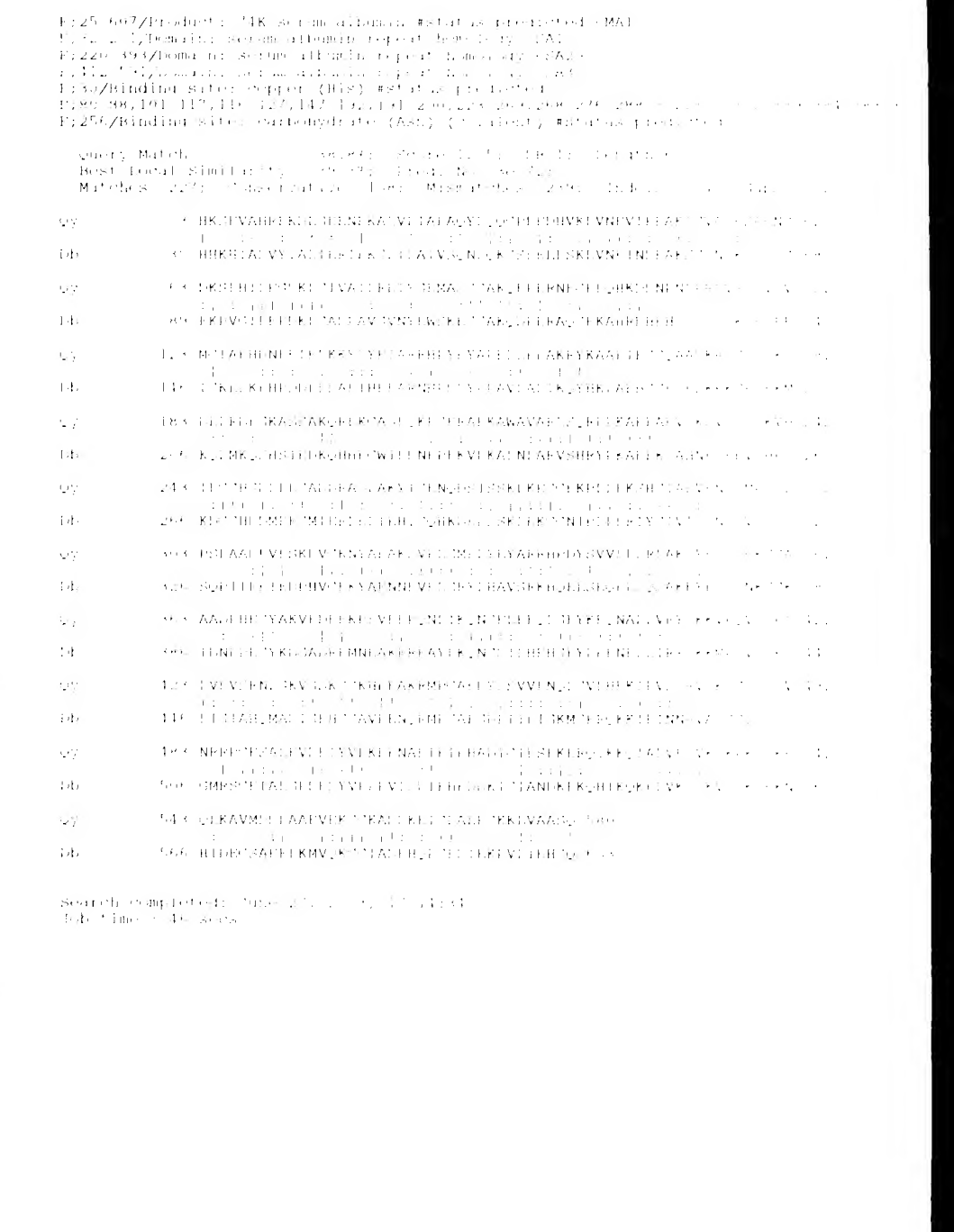
RESULT 13
FPHU
alpha-fetoprotein precursor [validated] - human
N;Alternate names: AFP; alpha-1-fetoprotein; alpha-fetoglobulin
C;Species: Homo sapiens (man)
C;Date: [illegible] #sequence_revision [illegible] #text_change [illegible]
C;Accession: A26621; [illegible]; A[illegible]; A[illegible]; A[illegible]; A61486; A[illegible]
R;Gibbs, P.E.M.; Zielinski, R.; Boyd, C.; Dugaiczyk, A.
Biochemistry 26, 1332-1343, 1987
A;Title: Structure, polymorphism, and novel repeated DNA [illegible]
A;Reference number: A26621; MUID:[illegible]; PMID:[illegible]
A;Accession: A26621
A;Molecule type: DNA
A;Residues: 1-609 <GIB>
A;Cross-references: GB:M16110; NID:[illegible]; PIDN:AAB[illegible]
R;McVey, J.H.; Michaelides, K.; Hansen, L.P.; Ferguson-Smith, M.[illegible]
Hum. Mol. Genet. 2, [illegible], 1993
A;Title: A G-A substitution in an HNF-1 binding site in the human [illegible]
A;Reference number: [illegible]; PMID:[illegible]
A;Accession: S[illegible]
A;Molecule type: DNA
A;Residues: 1-28 <MCV>
A;Cross-references: EMBL:[illegible]; NID:[illegible]; PIDN:CAA[illegible]
A;Note: the authors translated the codon [illegible] for residue [illegible]
R;Morinaga, T.; Sakai, M.; Wegmann, T.G.; Tamaoki, T.
Proc. Natl. Acad. Sci. U.S.A. 80, [illegible], 1983
A;Title: Primary structures of human alpha-fetoprotein and its mRNA
A;Reference number: A[illegible]; MUID:[illegible]; PMID:[illegible]
A;Accession: A[illegible]
A;Molecule type: mRNA
A;Residues: 1-609 <MOR>
A;Cross-references: GB:[illegible]; NID:[illegible]; PIDN:AAA24777.1; PID:[illegible]
R;Beattie, W.G.; Dugaiczyk, A.
Gene 20, 415-422, 1982
A;Title: Structure and evolution of human alpha-fetoprotein deduced [illegible]
A;Reference number: A91497; MUID:83150726; PMID:[illegible]
A;Accession: A91497
A;Molecule type: mRNA
A;Residues: 429-556 <BEA>
A;Cross-references: GB:[illegible]
R;Pucci, P.; Siciliano, R.; Malorni, A.; Marino, G.; [illegible]
Biochemistry 30, 5061-5066, 1991
A;Title: Human alpha-fetoprotein primary structure: a mass spectrometric [illegible]
A;Reference number: A[illegible]; MUID:[illegible]; PMID:[illegible]
A;Accession: A26[illegible]
A;Molecule type: protein
A;Residues: 19-45;69-[illegible]
R;Leffe, M.F.; Terrana, B.; Carlsen, M.M.; Ceccarini, C.
J. Natl. Med. Allied Sci. 41, 213-216, 1990
A;Title: Characterization of in vitro expressed human alpha-fetoprotein [illegible]
A;Reference number: A61486; MUID:[illegible]; PMID:[illegible]
A;Accession: A61486
A;Molecule type: protein









OM protein - protein search, using sw model

Run on: June 27, 2003, 1[illegible]:59:[illegible] ; Search time 25 Seconds
(without alignments)
970.54[illegible] Million cell updates/sec

Title: US-09-832-501-18
Perfect score: 510[illegible]
Sequence: 1 DAHK[illegible]VAHRFKD[illegible]ENFK..........[illegible]AAS[illegible]KKLVAA[illegible]AAL[illegible]L 58[illegible]

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 4147[illegible]828 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt 40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5103	100.0	609	1	ALBU_HUMAN	P02768 homo sapien
2	2942	94.8	600	1	ALBU_MACMU	Q28522 macaca mula
3	2620	84.4	608	1	ALBU_FELCA	P49064 felis silve
4	2562	82.6	608	1	ALBU_CANFA	P49822 canis famil
5	2475.5	79.8	607	1	ALBU_HORSE	P35747 equus cabal
6	24[illegible].5	79.[illegible]	607	1	ALBU_BOVIN	P02769 bos taurus
7	2446	78.8	608	1	ALBU_RABIT	P49065 oryctolagus
8	2432.5	78.4	607	1	ALBU_SHEEP	P14639 ovis aries
9	2426	78.2	608	1	ALBU_RAT	P02770 rattus norv
10	2411.5	77.7	605	1	ALBU_PIG	P08835 sus scrofa
11	238[illegible]	7[illegible]	609	1	ALBU_MERUN	O35090 meriones un
12	2378	76.6	608	1	ALBU_MOUSE	P07724 mus musculu
13	155[illegible]	50.2	615	1	ALBU_CHICK	P19121 gallus gall
14	1253.5	40.4	609	1	FETA_PANTR	Q28789 pan troglod
15	1249.5	40.3	609	1	FETA_HUMAN	P02771 homo sapien
16	1242.5	40.[illegible]	609	1	FETA_GORGO	P28059 gorilla gor
17	1205	38.8	607	1	ALB2_XENLA	P14872 xenopus lae
18	1200	38.7	609	1	FETA_HORSE	P49066 equus cabal
19	1164.5	37.5	606	1	ALB1_XENLA	P08759 xenopus lae
20	1084	34.9	605	1	FETA_MOUSE	P02772 mus musculu
21	1067	34.4	611	1	FETA_RAT	P02773 rattus norv
22	105[illegible]	34.[illegible]	599	1	AFAM_HUMAN	P43652 homo sapien
23	944	30.4	611	1	AFAM_MOUSE	O89020 mus musculu
24	928	29.9	608	1	AFAM_RAT	P36953 rattus norv
25	747.5	24.1	608	1	ALB1_SALSA	P21848 salmo salar
26	742.5	23.9	608	1	ALB2_SALSA	Q03156 salmo salar
27	699	22.5	382	1	ALBU_RANCA	P21847 rana catesb
28	440.5	14.2	1423	1	ALBU_PETMA	Q91274 petromyzon
29	386	12.4	474	1	VTDB_HUMAN	P02774 homo sapien
30	381	12.3	476	1	VTDB_RAT	P04276 rattus norv
31	378	12.2	476	1	VTDB_RABIT	P53789 oryctolagus
32	372	12.0	472	1	VTDB_MOUSE	P21614 mus musculu
33	133.5	4.3	1391	1	MS12_DROHY	Q08696 drosophila

Result No.	Score	% Query Match	Length	DB	ID	Description
34	13[illegible]	4.[illegible]	[illegible]	1	[illegible]_HUMAN	[illegible]
35	129.5	4.[illegible]	1[illegible]	1	MYH[illegible]_HUMAN	[illegible]
36	12[illegible]	4.[illegible]	[illegible]	1	[illegible]_HUMAN	[illegible]
37	128	4.1	[illegible]	1	[illegible]_ME[illegible]A	[illegible]
38	12[illegible]	4.[illegible]	[illegible]	1	MYH[illegible]_RABIT	[illegible]
39	12[illegible]	4.[illegible]	[illegible]	1	[illegible]	[illegible]
40	12[illegible]	4.[illegible]	[illegible]	1	[illegible]_HUMAN	[illegible]
41	124.5	4.[illegible]	17[illegible]	1	[illegible]_YEAST	[illegible]
42	124	4.[illegible]	[illegible]	1	[illegible]_HUMAN	[illegible]
43	12[illegible]	4.[illegible]	[illegible]	1	[illegible]_HUMAN	[illegible]
44	12[illegible]	4.[illegible]	[illegible]	1	MYH[illegible]_RAT	[illegible]
45	122.5	[illegible]	[illegible]	1	[illegible]	[illegible]

ALIGNMENTS

RESULT 1
ALBU_HUMAN
ID ALBU_HUMAN STANDARD; PRT; [illegible] AA.
AC P02768; Q13140; [illegible]
DT 21-JUL-1986 (Rel. [illegible], Created)
DT 01-APR-19[illegible] (Rel. [illegible], Last sequence update)
DT 15-JUN-2002 (Rel. [illegible], Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196112; PubMed=[illegible];
RA Minghetti P.P., Ruffner D.E., Kuang W.-J., Dennison [illegible], [illegible] W.,
RA Beattie W.G., Dugaiczyk A.;
RT "Molecular structure of the human albumin gene is revealed by
RT nucleotide sequence within q11-22 of chromosome 4.";
RL J. Biol. Chem. 261:6747-6757(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=[illegible]; PubMed=[illegible];
RA Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,
RA Najarian R.C., Seeburg P.H., Wion K.L.;
RT "The sequence of human serum albumin cDNA and its expression in E.
RT coli.";
RL Nucleic Acids Res. [illegible](1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=[illegible]; PubMed=[illegible];
RA Dugaiczyk A., Law S.W., Dennison [illegible];
RT "Nucleotide sequence and the [illegible] human serum
RT albumin mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. [illegible](198[illegible]).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Yang S., Zhang R.A., [illegible] Y.[illegible];
RL Submitted (SEP-19[illegible]) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Zhang [illegible], Yu Y., Zhang [illegible], Wei [illegible], [illegible]
RA He F.;
RT "Functional prediction of the coding sequences of [illegible] new genes deduced
RT by analysis of cDNA clones from human fetal liver.";
RL Submitted (JAN-19[illegible]) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE OF 25-[illegible].
RX MEDLINE=76187907; PubMed=[illegible];
RA Meloun B., Moravek L., Kostka V.;
RT "Complete amino acid sequence of human serum albumin.";
RL FEBS Lett. 58:134-137(1975).
RN [7]

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RP   SEQUENCE OF 25-609.
RA   [illegible], Shockley P., Peters P.[illegible];
RL   (In) Bing D.H. (eds.);
RL   The chemistry and physiology of the human plasma proteins, pp.2[illegible]-40,
RL   Pergamon Press, New York (1979).
RN   [8]
RP   SEQUENCE OF 1-455 FROM N.A.
RC   TISSUE=Liver;
RA   Menaya J., Parrilla R., Ayuso M.S.;
RL   Submitted (MAR [illegible]) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   PARTIAL SEQUENCE FROM N.A. [illegible].
RC   TISSUE=Fetal liver;
RA   Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,
RA   Xu W., [illegible] F., Liu M., He F., Zhang Y., [illegible] C., [illegible] L.;
RT   "Functional prediction of the coding sequences of 121 new genes
RT   deduced by analysis of cDNA clones from human fetal liver.";
RL   Submitted ([illegible]) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   SEQUENCE OF 1-26 FROM N.A.
RX   MEDLINE=86140099; PubMed=2419329;
RA   Urano Y., Watanabe K., Sakai M., Tamaoki T.;
RT   "The human albumin gene. Characterization of the 5' and 3' flanking
RT   regions and the polymorphic gene transcripts.";
RL   J. Biol. Chem. 261:3244-3251(1986).
RN   [11]
RP   SEQUENCE OF 222-229.
RX   MEDLINE=7[illegible]; PubMed=[illegible];
RA   Walker J.E.;
RT   "Lysine residue 199 of human serum albumin is modified by
RT   acetylsalicyclic acid.";
RL   FEBS Lett. 66:173-175(1976).
RN   [12]
RP   SEQUENCE OF 25-44 AND 480-499.
RC   TISSUE=Heart;
RX   MEDLINE=95203287; PubMed=789[illegible];
RA   Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT   "The human myocardial two-dimensional gel protein database: update
RT   1994.";
RL   Electrophoresis 15:1459-1465(1994).
RN   [13]
RP   SEQUENCE OF 409-609 FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Strausberg R.;
RL   Submitted ([illegible]) to the EMBL/GenBank/DDBJ databases.
RN   [14]
RP   DISULFIDE BONDS.
RA   Saber M.A., Stockbauer P., Moravek L., Meloun B.;
RT   "Disulfide bonds in human serum albumin.";
RL   Collect. Czech. Chem. Commun. 42:564-579(1977).
RN   [15]
RP   BILIRUBIN BINDING SITE.
RX   MEDLINE=78186630; PubMed=656055;
RA   Jacobsen C.;
RT   "Lysine residue 240 of human serum albumin is involved in high-
RT   affinity binding of bilirubin.";
RL   Biochem. J. 171:453-459(1978).
RN   [16]
RP   VARIANT CANTERBURY.
RX   MEDLINE=87157744; PubMed=3828358;
RA   Brennan S.O., Herbert P.;
RT   "Albumin Canterbury (313 Lys-->Asn). A point mutation in the second
RT   domain of serum albumin.";
RL   Biochim. Biophys. Acta 912:191-197(1987).
RN   [17]
RP   VARIANTS NAG-2 AND NAG-3.
RX   MEDLINE=88068523; PubMed=3479777;
RA   Takahashi N., Takahashi Y., [illegible] I., Putnam F.W., Fujita M.,
RA   Satoh C., Neel J.V.;
RT   "Amino acid substitutions in inherited albumin variants from
RT   Amerindian and Japanese populations.";
RL   Proc. Natl. Acad. Sci. U.S.A. [illegible](1987).
RN   [18]
RP   VARIANTS NAG-1; HIR-1; HIR-2 AND [illegible].
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Arai K., Madison J., Huss K., Ishioka N., Satoh C., Fujita M.,
RA   Neel J.V., Sakurabayashi I., Putnam F.W.;
RT   "Point substitutions in Japanese alloalbumins.";
RL   Proc. Natl. Acad. Sci. U.S.A. [illegible](1989).
RN   [19]
RP   VARIANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW [illegible].
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Arai K., [illegible] Putnam F.W.;
RT   "Point substitutions in albumin genetic variants from Asia.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:[illegible](1990).
RN   [20]
RP   VARIANT REDHILL.
RX   MEDLINE=[illegible]; PubMed=2104980;
RA   Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
RT   "Albumin Redhill ([illegible] Arg, 320 Ala-->Thr): a glycoprotein variant [illegible]
RT   [illegible] precursor has an aberrant signal [illegible]
RT   cleavage site.";
RL   Proc. Natl. Acad. Sci. U.S.A. [illegible](1990).
RN   [21]
RP   VARIANTS [illegible] AND VIC-VALENTIA.
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Mad[illegible],
RA   Watkins S., Putnam F.W.;
RT   "Mutations in genetic variants of human serum albumin found in
RT   Italy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:[illegible](1990).
RN   [22]
RP   VARIANT VENEZIA.
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
RA   Minchiotti L., Putnam F.W.;
RT   "A donor splice mutation and a single-base deletion produce two
RT   carboxyl-terminal variants of human serum albumin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
RN   [23]
RP   VARIANTS IOWA CITY AND K-MAG ME.
RX   MEDLINE=9205218[illegible]; PubMed=[illegible];
RA   Madison J., Arai K., [illegible], Kyle R.A., Watkins S., [illegible]
RA   Matsuda Y., [illegible], Amaki [illegible], Putnam F.W.;
RT   "Genetic variants of serum albumin in Americans and Japanese.";
RL   Proc. Natl. Acad. Sci. U.S.A. [illegible](1991).
RN   [24]
RP   VARIANT [illegible].
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Peach R.J., Brennan S.O.;
RT   "Structural characterization of a glycoprotein variant of human serum
RT   albumin: albumin Casebrook (494 Asp-->Asn).";
RL   Biochim. Biophys. Acta 1097:[illegible](1991).
RN   [25]
RP   VARIANTS [illegible] AND PARIS-2.
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
RA   Rochu D., Porta F.;
RT   "Two alloalbumins with identical electrophoretic mobility are produced
RT   by differently charged amino acid substitutions.";
RL   Biochim. Biophys. Acta 1119:[illegible](1992).
RN   [26]
RP   VARIANTS MALMO.
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Carlson J., Sakamoto Y., Laurell C.-B., Madison J., Watkins S.,
RA   Putnam F.W.;
RT   "Alloalbuminemia in Sweden: structural study and phenotypic
RT   distribution of nine albumin variants.";
RL   Proc. Natl. Acad. Sci. U.S.A. [illegible](1992).
RN   [27]
RP   VARIANT HERBORN.
RX   MEDLINE=93292504; PubMed=[illegible];
RA   Minchiotti L., Galliano M., Zapponi M.C., Tenni R.;
RT   "The structural characterization and bilirubin-binding properties of
RT   albumin Herborn, a [Lys240-->Glu] albumin mutant.";
RL   Eur. J. Biochem. 214:[illegible](1993).
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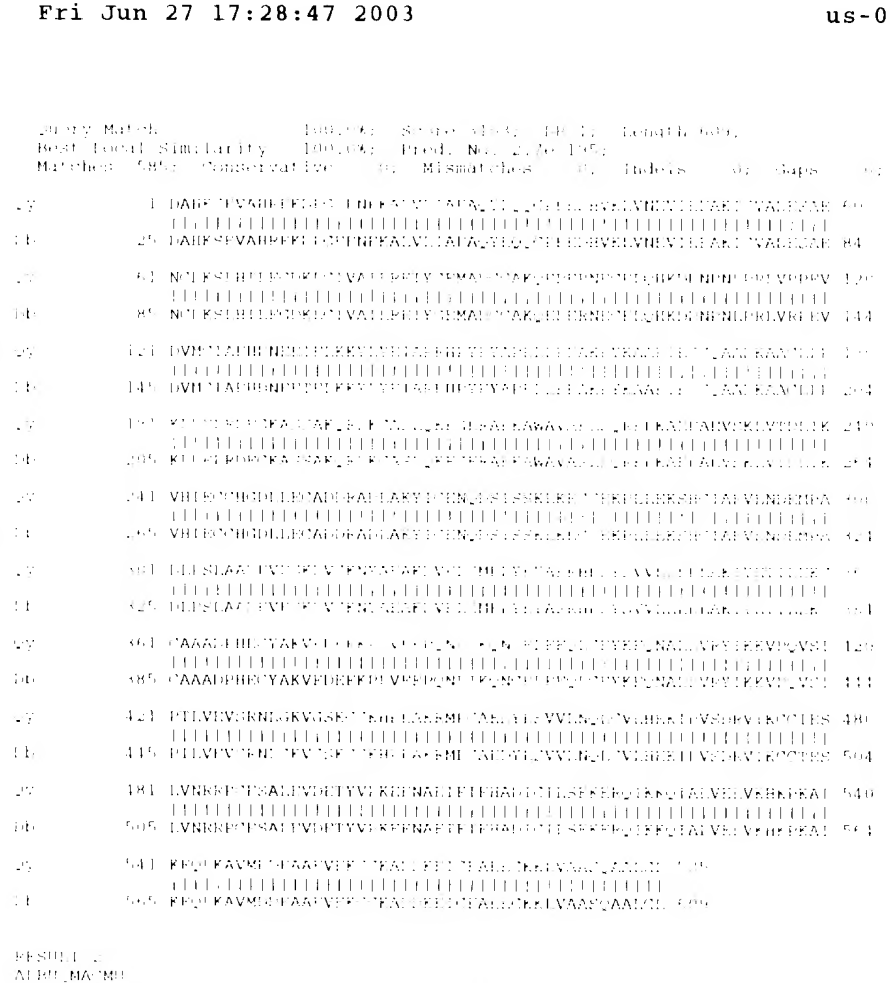

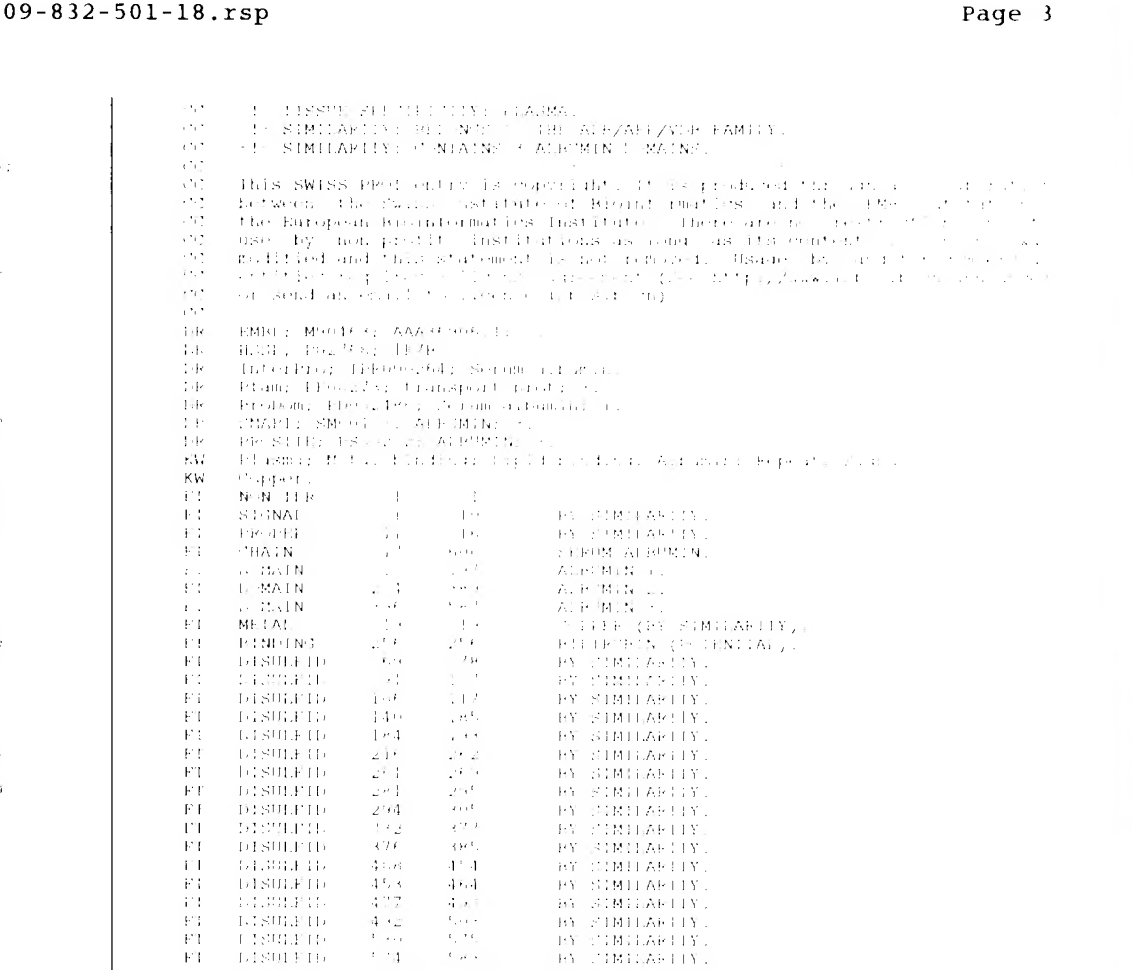

RESULT 3
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ID ALBU_FELCA STANDARD; PRT; 608 AA.
AC P49064;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Allergen Fel d 2).
GN ALB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96194823; PubMed=8624427;
RA Bilgic C., Griglioni F., Kohnen M., Bontjes F.;
RT "Sequence of the gene encoding cat (Felis domesticus) serum albumin.";
RL Gene 169:295-296(1996).
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A HIGH
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALBUMIN/AFP FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X84842; CAA59279.1; -.
DR HSSP; P02768; 1E7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00274; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper; Allergen.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 608 SERUM ALBUMIN.
FT DOMAIN 25 285 ALBUMIN 1.
FT DOMAIN 272 397 ALBUMIN 2.
FT DOMAIN 404 595 ALBUMIN 3.
FT MISC. 27 27 CYS-34.
FT DISULFID 44 44 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 126 BY SIMILARITY.
FT DISULFID 148 160 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 247 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 284 299 BY SIMILARITY.
FT DISULFID 302 329 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 399 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 464 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 560 511 BY SIMILARITY.
FT DISULFID 529 582 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
SQ SEQUENCE 608 AA; MW; 67E6J9CA 5F60E5EC CRC64;

Query Match: 41.4%; Score 208; DB 1; Length
Best Local Similarity 42.0%; Pred. No. 4e-164;
Matches 429; Conservative 0; Mismatches 53; Indels 2; Gaps

RESULT 4
ALBU_CANFA
ID ALBU_CANFA STANDARD; PRT; 609 AA.
AC P49822;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Allergen Can f 2).

```
GN   ALB.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Beagle; TISSUE=Liver;
RA   Hilger C.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20148667; PubMed=10673848;
RA   Pandjaitan B., Swoboda I., Brandejsky-Pichler F., Rumpold H.,
RA   Valenta R., Spitzauer S.;
RT   "Escherichia coli expression and purification of recombinant dog
RT   albumin, a cross-reactive animal allergen.";
RL   J. Allergy Clin. Immunol. 105:279-285(2000).
RN   [3]
RP   SEQUENCE OF 25-48.
RX   MEDLINE=75011422; PubMed=4414013;
RA   Dixon J.W., Sarkar B.;
RT   "Isolation, amino acid sequence and copper(II)-binding properties of
RT   peptide (1-24) of dog serum albumin.";
RL   J. Biol. Chem. 249:5872-5877(1974).
RN   [4]
RP   SEQUENCE OF 25-48.
RC   TISSUE=Heart;
RX   MEDLINE=98163340; PubMed=9504812;
RA   Dunn M.J., Corbett J.M., Wheeler C.H.;
RT   "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT   dog heart proteins.";
RL   Electrophoresis 18:2795-2802(1997).
RN   [5]
RP   SEQUENCE OF 215-478 FROM N.A.
RC   TISSUE=Salivary gland;
RX   MEDLINE=94201492; PubMed=7512102;
RA   Spitzauer S., Schweiger C., Sperr W.R., Pandjaitan B., Valent P.,
RA   Muehl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;
RT   "Molecular characterization of dog albumin as a cross-reactive
RT   allergen.";
RL   J. Allergy Clin. Immunol. 93:614-627(1994).
CC   -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC       BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC       BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC       COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC   --------------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AJ133489; CAB64867.1; -.
DR   EMBL; Y17737; CAA76941.1; -.
DR   EMBL; S72946; AAB30434.1; -.
DR   PIR; S29749; S29749.
DR   HSSP; P02768; 1E7H.
DR   HSC-2DPAGE; P49822; DOG.
DR   InterPro; IPR000264; Serum_albumin.
DR   Pfam; PF00273; transport_prot; 3.
DR   PRINTS; PR00802; SERUMALBUMIN.
DR   ProDom; PD002486; Serum_albumin; 1.
DR   SMART; SM00103; ALBUMIN; 3.
DR   PROSITE; PS00212; ALBUMIN; 3.
KW   Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW   Copper; Allergen.
FT   SIGNAL        1     18       POTENTIAL.
FT   PROPEP       19     24
FT   CHAIN        25    608       SERUM ALBUMIN.
FT   DOMAIN       25    209       ALBUMIN 1.
FT   DOMAIN      210    402       ALBUMIN 2.
FT   DOMAIN      403    600       ALBUMIN 3.
FT   METAL        27     27       COPPER (BY SIMILARITY).
FT   DISULFID     77     86       BY SIMILARITY.
FT   DISULFID     99    115       BY SIMILARITY.
FT   DISULFID    114    125       BY SIMILARITY.
FT   DISULFID    148    193       BY SIMILARITY.
FT   DISULFID    192    201       BY SIMILARITY.
FT   DISULFID    224    270       BY SIMILARITY.
FT   DISULFID    269    277       BY SIMILARITY.
FT   DISULFID    289    303       BY SIMILARITY.
FT   DISULFID    302    313       BY SIMILARITY.
FT   DISULFID    340    385       BY SIMILARITY.
FT   DISULFID    384    393       BY SIMILARITY.
FT   DISULFID    416    462       BY SIMILARITY.
FT   DISULFID    461    472       BY SIMILARITY.
FT   DISULFID    485    501       BY SIMILARITY.
FT   DISULFID    500    511       BY SIMILARITY.
FT   DISULFID    538    583       BY SIMILARITY.
FT   DISULFID    582    591       BY SIMILARITY.
FT   CONFLICT      1     25       MKWVTFISLLLLFSSAYSRGVFRRA -> [illegible]
FT                                REF. 2).
FT   CONFLICT    [illegible] [illegible]  A -> R (IN REF. 2).
FT   CONFLICT    [illegible] [illegible]  [illegible] -> [illegible] (IN REF. [illegible]).
FT   CONFLICT    [illegible] [illegible]  V -> A (IN REF. [illegible]).
FT   CONFLICT    [illegible] [illegible]  S -> A (IN REF. 5).
FT   CONFLICT    448    449       V -> VV (IN REF. 5).
FT   CONFLICT    473    474       [illegible] -> [illegible] (IN REF. 5).
SQ   SEQUENCE   608 AA;  [illegible] MW;  [illegible] CRC64;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 608;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  465;  Conservative  [illegible];  Mismatches  [illegible];  Indels [illegible];  Gaps [illegible];

Qy          1 [illegible]
Db         25 [illegible]

Qy         61 [illegible]
Db         85 [illegible]

Qy        121 [illegible]
Db        145 [illegible]

Qy        181 [illegible]
Db        205 [illegible]

Qy        241 [illegible]
Db        265 [illegible]

Qy        301 [illegible]
Db        325 [illegible]

Qy        361 [illegible]
Db        385 [illegible]

Qy        421 [illegible]
Db        445 [illegible]

Qy        481 [illegible]
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RESULT 5
ALBU_HORSE STANDARD; PRT; 607 AA.
AC P35747;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A., AND N-TERMINAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=93345465; PubMed=8344282;
RA Peters T. Jr., Brown J.R., Carter D.C.;
RT "X-ray and primary structure of horse serum albumin (Equus caballus)
RT at 0.27-nm resolution.";
RL Eur. J. Biochem. 215:205-212(1993);
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HEMIN AND
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALBUMIN/AFP/VDB FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC --
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CC --
DR EMBL; X74045; CAA52194.1; -.
DR PIR; S44953; ABHOS.
DR HSSP; P02768; 1E7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot, 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002499; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 607 SERUM ALBUMIN.
FT DOMAIN 25 204 ALBUMIN 1.
FT DOMAIN 211 396 ALBUMIN 2.
FT DOMAIN 403 591 ALBUMIN 3.
FT METAL 27 27 COPPER (BY SIMILARITY).
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 147 192
FT DISULFID 191 280
FT DISULFID 223 269
FT DISULFID 268 276
FT DISULFID 288 302
FT DISULFID 301 312
FT DISULFID 389 484
FT DISULFID 483 492
FT DISULFID 497 506
FT DISULFID 505 513
FT DISULFID 517 580
FT DISULFID 581 590
SQ SEQUENCE 607 AA; 68809 MW; [illegible] CRC64;

Query Match [illegible]; Score [illegible]; DB 1; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

RESULT 6
ALBU_BOVIN
ID ALBU_BOVIN STANDARD; PRT; [illegible] AA.
AC P02769; Q02787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Albumin Bos d 6).
GN ALB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Holowachuk E.W., Strollentrein J.K., Reed K.C., Peters J. Jr.;
RL Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Barry T., Power S., Gannon F.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE OF 1-32.
RX MEDLINE=80024278; PubMed=499709;
RA MacGillivray R.T.A., Chung D.W., Davie E.W.;
RT "Biosynthesis of bovine plasma proteins in a cell-free system. Amino-
RT terminal sequence of preproalbumin.";
RL Eur. J. Biochem. 98:477-485(1979).
RN [7]
RP SEQUENCE OF 25-424 AND 429-607.
RA Brown J.R.;
RT "Structure of bovine serum albumin.";
RL Fed. Proc. 34:591-591(1975).
RN [8]
RP REVISIONS TO 190-196.
RA Brown J.R.;
RL Submitted (APR-1975) to the PIR data bank.
RN [9]
RP SEQUENCE OF 402-433.
RX MEDLINE=82023364; PubMed=7283978;
RA Reed R.G., Putnam F.W., Peters T. Jr.;
RT "Sequence of residues 400-403 of bovine serum albumin.";
RL Biochem. J. 191:867-868(1980).
RN [10]
RP SEQUENCE OF 19-28.
RX MEDLINE=77134075; PubMed=843354;
RA Patterson J.E., Geller D.M.;
RT "Bovine microsomal albumin: amino terminal sequence of bovine
RT proalbumin.";
RL Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
RN [11]
RP SEQUENCE, AND REVISIONS TO 118-119 AND 199.
RX MEDLINE=91083649; PubMed=2260975;
RA Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
RT "Rapid confirmation and revision of the primary structure of bovine
RT serum albumin by ESIMS and Frit-FAB LC/MS.";
RL Biochem. Biophys. Res. Commun. 173:639-646(1990).
RN [12]
RP SEQUENCE OF 25-41.
RX MEDLINE=88267456; PubMed=3389500;
RA Hsieh J.C., Lin F.P., Tam M.F.;
RT "Electroblotting onto glass-fiber filter from an analytical
RT isoelectrofocusing gel: a preparative method for isolating proteins
RT for N-terminal microsequencing.";
RL Anal. Biochem. 170:1-8(1988).
RN [13]
RP SEQUENCE OF 437-451.
RA Vilbois F.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.
RN [14]
RP DISULFIDE BONDS.
RA Brown J.R.;
RT "Structure of serum albumin: disulfide bridges.";
RL Fed. Proc. 33:1389-1389(1974).
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC --
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CC modified and this statement is not removed. [illegible]
CC [illegible]
CC or send an email to [illegible]).
CC --
DR EMBL; M73993; AAA51411.1; -.
DR EMBL; X58989; CAA41735.1; -.
DR EMBL; Y17769; CAA76847.1; -.
DR PIR; A38885; ABBOS.
DR HSSP; P02768; 1BJ5.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; Serum_albumin; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD000461; Serum_albumin; 3.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Albumin; Metal-binding; Lipid-binding; Repeat; Signal;
KW Copper; Allergen.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 607 SERUM ALBUMIN.
FT DOMAIN 25 [illegible] ALBUMIN 1.
FT DOMAIN [illegible] [illegible] ALBUMIN 2.
FT DOMAIN [illegible] [illegible] ALBUMIN 3.
FT METAL 27 27 COPPER (BY SIMILARITY).
FT DISULFID [illegible] [illegible]
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FT DISULFID 123 [illegible]
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FT DISULFID 288 [illegible]
FT DISULFID [illegible] [illegible]
FT DISULFID [illegible] 391
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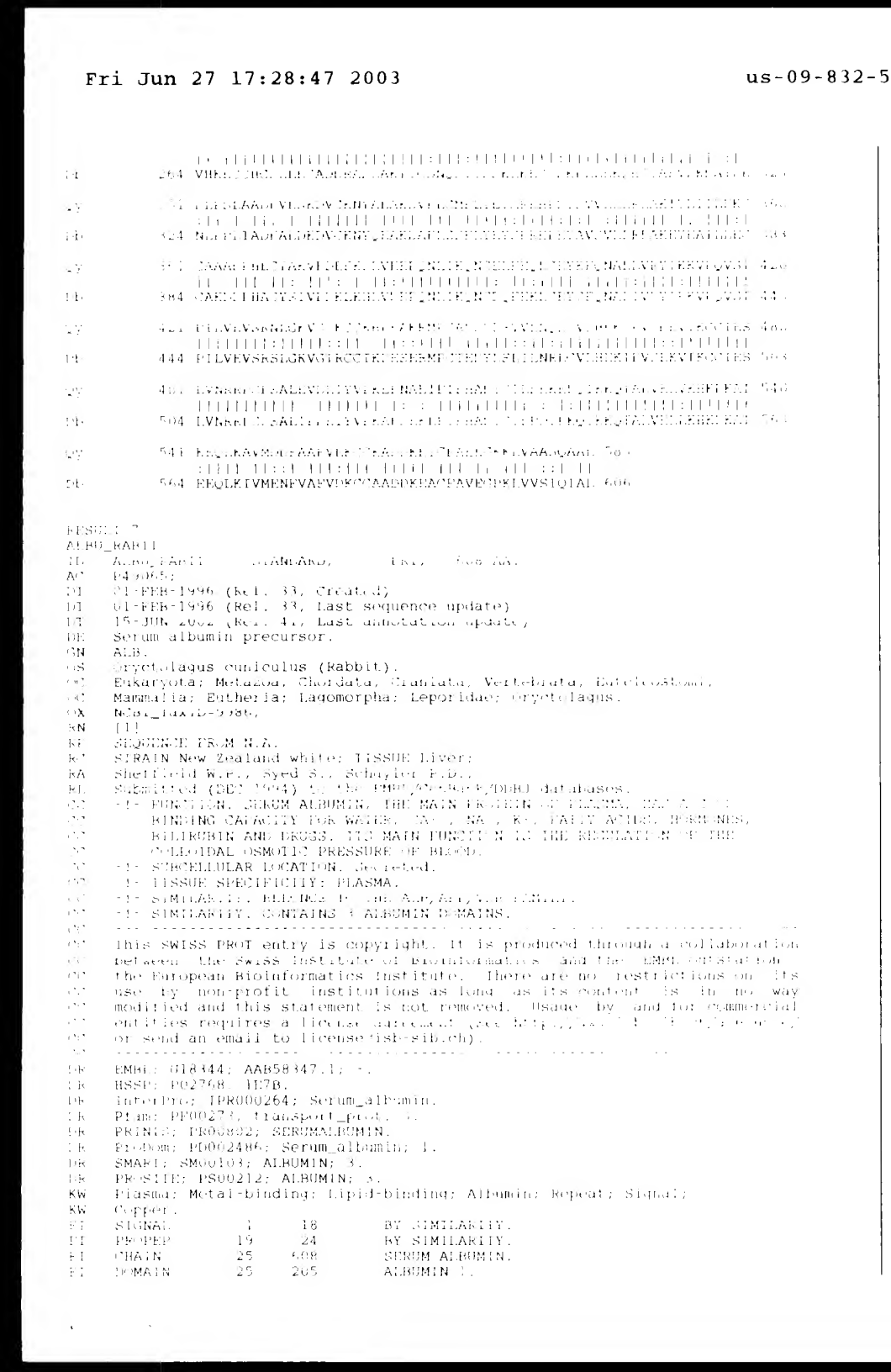
FT DISULFID 437 [illegible]
FT DISULFID 460 [illegible]
FT DISULFID 484 [illegible]
FT DISULFID 499 [illegible]
FT DISULFID 5?7 [illegible]
FT DISULFID 58? [illegible]
FT CONFLICT 214 214 A -> [illegible] (IN REF. 2 AND 5).
FT CONFLICT 302 302 [illegible] -> K (IN REF. 5).
FT CONFLICT 304 305 KP -> [illegible] (IN REF. 5).
FT CONFLICT 324 324 N -> [illegible] (IN REF. 5).
FT CONFLICT 394 395 [illegible] -> [illegible]S (IN REF. 5).
FT CONFLICT 437 437 K -> [illegible] (IN REF. 11).
FT CONFLICT 493 494 SE -> [illegible] (IN REF. 5).
SQ SEQUENCE 607 AA; [illegible] MW; [illegible] CRC64;

Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 442; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy 1 DAHKSEVAHRFKD[illegible]ENFKALVLIAFAQYLQQ[illegible]FEDHVKLVNEVTEFAK[illegible]
Db 25 DTHKSEIAHRFKDLGEEHFKGLVLIAFSQYLQQCPFDEHVKLVNELTEFAK[illegible]
Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV[illegible]
Db 85 [illegible]LHTLFGDELCKVASLRETYGDMADCCEKQEPERNECFLSHKDDSPDLPKLKPDPN[illegible]
Qy 121 [illegible]
Db 145 [illegible]
Qy 181 [illegible]
Db 204 [illegible]
Qy 241 [illegible]



RESULT 7
ALBU_RABIT
ID ALBU_RABIT STANDARD; PRT; 606 AA.
AC P49065;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN New Zealand white; TISSUE Liver;
RA Sheffield W.E., Syed S., Schuyler E.D.,
RL Submitted (SEP 1994) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A [illegible]
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. IT'S MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: BELONGS TO THE ALBUMIN FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC ---------- [illegible]
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CC or send an email to license@isb-sib.ch).
CC ---------- [illegible]
DR EMBL; U18344; AAB58347.1; -.
DR HSSP; P02768; 1E7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; Transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 609 SERUM ALBUMIN.
FT DOMAIN 25 205 ALBUMIN 1.
FT DOMAIN 206 403 ALBUMIN 2.
FT DOMAIN 404 606 ALBUMIN 3.
FT METAL 27 27 COPPER.
FT DISULFID 32 36 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 103 125 BY SIMILARITY.
FT DISULFID 119 193 BY SIMILARITY.
FT DISULFID 179 [illegible] BY SIMILARITY.
FT DISULFID 201 220 BY SIMILARITY.
FT DISULFID 214 227 BY SIMILARITY.
FT DISULFID 289 308 BY SIMILARITY.
FT DISULFID 302 [illegible] BY SIMILARITY.
FT DISULFID 340 365 BY SIMILARITY.
FT DISULFID 381 [illegible] BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 451 472 BY SIMILARITY.
FT DISULFID 496 501 BY SIMILARITY.
FT DISULFID [illegible] [illegible] BY SIMILARITY.
FT DISULFID 508 563 BY SIMILARITY.
FT DISULFID [illegible] [illegible] BY SIMILARITY.
SQ SEQUENCE 609 AA; 68911 MW; [illegible] CRC64;

Query Match [illegible]; Score 2147; DB 1; Length [illegible];
Best Local Similarity 71.7%; Pred. No. 1.2e-152;
Matches 433; Conservative 77; Mismatches 74; Indels [illegible]; Gaps [illegible];

RESULT 8
ALBU_SHEEP
ID ALBU_SHEEP STANDARD; PRT; [illegible] AA.
AC P14639;
DT 01-APR-1990 (Rel. 11, Created)
DT 01-APR-1990 (Rel. 11, Last sequence update)

```
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Serum albumin precursor.
GN   ALB.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=90098888; PubMed=2602160;
RA   Brown W.M., Dziegielewska K.M., Foreman R.C., Saunders N.R.;
RT   "Nucleotide and deduced amino acid sequence of sheep serum albumin.";
RL   Nucleic Acids Res. 17:10495-10495(1989).
CC   -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC       BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC       BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC       COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC   --------------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no way
CC   modified and this statement is not removed.  Usage  by  and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X17055; CAA34903.1; -.
DR   PIR; S06936; ABSHS.
DR   HSSP; P02768; 1E7B.
DR   InterPro; IPR000264; Serum_albumin.
DR   Pfam; PF00273; transport_prot; 3.
DR   PRINTS; PR00802; SERUMALBUMIN.
DR   ProDom; PD002486; Serum_albumin; 1.
DR   SMART; SM00103; ALBUMIN; 3.
DR   PROSITE; PS00212; ALBUMIN; 3.
KW   Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW   Copper.
FT   SIGNAL        1     18       BY SIMILARITY.
FT   PROPEP       19     24       BY SIMILARITY.
FT   CHAIN        25    607       SERUM ALBUMIN.
FT   DOMAIN       25    204       ALBUMIN 1.
FT   DOMAIN      211    396       ALBUMIN 2.
FT   DOMAIN      403    594       ALBUMIN 3.
FT   METAL        27     27       COPPER (BY SIMILARITY).
FT   DISULFID     77     86       BY SIMILARITY.
FT   DISULFID     99    115       BY SIMILARITY.
FT   DISULFID    114    125       BY SIMILARITY.
FT   DISULFID    147    192       BY SIMILARITY.
FT   DISULFID    191    200       BY SIMILARITY.
FT   DISULFID    223    269       BY SIMILARITY.
FT   DISULFID    268    276       BY SIMILARITY.
FT   DISULFID    288    302       BY SIMILARITY.
FT   DISULFID    301    312       BY SIMILARITY.
FT   DISULFID    339    384       BY SIMILARITY.
FT   DISULFID    383    392       BY SIMILARITY.
FT   DISULFID    415    461       BY SIMILARITY.
FT   DISULFID    460    471       BY SIMILARITY.
FT   DISULFID    484    500       BY SIMILARITY.
FT   DISULFID    499    510       BY SIMILARITY.
FT   DISULFID    547    592       BY SIMILARITY.
FT   DISULFID    591    600       BY SIMILARITY.
SQ   SEQUENCE   607 AA;  69188 MW;  84979A87F8B86596 CRC64;

  Query Match             78.4%;  Score 2432.5;  DB 1;  Length 607;
  Best Local Similarity   75.0%;  Pred. No. 1.4e-151;
  Matches  437;  Conservative   73;  Mismatches   72;  Indels    1;  Gaps    1;

Qy          1 [illegible]
Db         25 [illegible]

Qy         61 [illegible]
Db         85 [illegible]

Qy        121 [illegible]
Db        144 [illegible]

Qy        181 [illegible]
Db        204 [illegible]

Qy        241 [illegible]
Db        264 [illegible]

Qy        301 [illegible]
Db        324 [illegible]

Qy        361 [illegible]
Db        384 [illegible]

Qy        421 [illegible]
Db        444 [illegible]

Qy        481 [illegible]
Db        504 [illegible]

Qy        541 [illegible]
Db        564 [illegible]


RESULT 4
ALBU_RAT
ID   ALBU_RAT       STANDARD;      PRT;   608 AA.
AC   P02770; [illegible]
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Serum albumin precursor [illegible]
GN   ALB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC   Mammalia; Eutheria; Rodentia; [illegible] Muridae; Murinae; [illegible]
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=[illegible]; PubMed=[illegible]
RA   Sargent T.D., Yang M., Bonner J.;
RT   "Nucleotide sequence of cloned rat serum albumin [illegible]"
RL   Proc. Natl. Acad. Sci. U.S.A. [illegible]
RN   [2]
RP   SEQUENCE OF 1-39, AND [illegible]
RX   MEDLINE=77219617; PubMed=[illegible]
RA   Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
RT   "Rat liver pre-proalbumin: complete amino acid sequence of the pre-
RT   piece. Analysis of the direct translation product of albumin
RT   messenger RNA.";
RL   J. Biol. Chem. 252:6846-6855(1977).
RN   [3]
RP   SEQUENCE OF 25-222.
RX   MEDLINE=78109429; PubMed=[illegible]
RA   Isemura S., Ikenaka T.;
RT   "Amino acid sequences of fragments I and II [illegible]
```

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RT   bromide cleavage of rat serum albumin.";
RL   J. Biochem. 83:35-48(1978).
RN   [4]
RP   SEQUENCE OF 223-288 AND 572-608.
RX   MEDLINE 76260153; PubMed=956149;
RA   Isemura S., Ikenaka T.;
RT   "Fragmentation of rat serum albumin by cyanogen bromide cleavage and
RT   the amino acid sequences of four fragments.";
RL   J. Biochem. 79:1183-1196(1976).
RN   [5]
RP   SEQUENCE OF 166-174.
RC   TISSUE=Plasma;
RX   MEDLINE 87194805; PubMed=2437111;
RA   Carraway R.E., Mitra S.P., Cochrane D.E.;
RT   "Structure of a biologically active neurotensin-related peptide
RT   obtained from pepsin-treated albumin(s).";
RL   J. Biol. Chem. 262:5968-5973(1987).
RN   [6]
RP   COPPER BINDING.
RX   MEDLINE [illegible]; PubMed=[illegible];
RA   Aoyagi Y., Ikenaka T., Ichida F.;
RT   "Copper(II)-binding ability of human alpha-fetoprotein.";
RL   Cancer Res. 38:3483-3486(1978).
CC   -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC       BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC       BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC       COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC   -!- FUNCTION: NRP REGULATES FAT DIGESTION, LIPID ABSORPTION, AND
CC       BLOOD FLOW (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC   --------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; V01222; CAA24532.1; -.
DR   PIR; A03233; ABRTS.
DR   HSSP; P02768; 1E7B.
DR   InterPro; IPR000264; Serum_albumin.
DR   Pfam; PF00273; transport_prot; 3.
DR   PRINTS; PR00802; SERUMALBUMIN.
DR   ProDom; PD002486; Serum_albumin; 1.
DR   SMART; SM00103; ALBUMIN; 3.
DR   PROSITE; PS00212; ALBUMIN; 3.
KW   Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW   Copper.
FT   SIGNAL        1     18
FT   PROPEP       19     24
FT   CHAIN        25    608       SERUM ALBUMIN.
FT   PEPTIDE     166    174       NEUROTENSIN-RELATED PEPTIDE.
FT   DOMAIN       25    205       ALBUMIN 1.
FT   DOMAIN      212    397       ALBUMIN 2.
FT   DOMAIN      404    595       ALBUMIN 3.
FT   METAL        27     27       COPPER.
FT   DISULFID     77     86       BY SIMILARITY.
FT   DISULFID     99    115       BY SIMILARITY.
FT   DISULFID    114    125       BY SIMILARITY.
FT   DISULFID    148    193       BY SIMILARITY.
FT   DISULFID    192    201       BY SIMILARITY.
FT   DISULFID    224    270       BY SIMILARITY.
FT   DISULFID    269    277       BY SIMILARITY.
FT   DISULFID    289    303       BY SIMILARITY.
FT   DISULFID    302    313       BY SIMILARITY.
FT   DISULFID    340    385       BY SIMILARITY.
FT   DISULFID    384    393       BY SIMILARITY.
FT   DISULFID    416    462       BY SIMILARITY.
FT   DISULFID    461    472       BY SIMILARITY.
FT   DISULFID    485    501       BY SIMILARITY.
FT   DISULFID    500    511       BY SIMILARITY.
FT   DISULFID    538    583       BY SIMILARITY.
FT   DISULFID    582    591       BY SIMILARITY.
FT   VARIANT     262    262       V -> I.
FT   CONFLICT    174    174       Y -> L (IN REF. 5).
SQ   SEQUENCE   608 AA;  [illegible] MW;  [illegible] CRC64;

  Query Match             78.2%;  Score 2420;  DB 1;  Length [illegible];
  Best Local Similarity   75.4%;  Pred. No. 3.7e-151;
  Matches  [illegible];  Conservative   82;  Mismatches   73;  Indels   [illegible];  Gaps   [illegible];

Qy          1 [illegible]
Db         25 [illegible]

Qy         61 [illegible]
Db         85 [illegible]

Qy        121 [illegible]
Db        145 [illegible]

Qy        181 [illegible]
Db        205 [illegible]

Qy        241 [illegible]
Db        265 [illegible]

Qy        301 [illegible]
Db        325 [illegible]

Qy        361 [illegible]
Db        385 [illegible]

Qy        421 [illegible]
Db        445 [illegible]

Qy        481 [illegible]
Db        505 [illegible]

Qy        541 [illegible]
Db        565 [illegible]


RESULT 18
ALBU_PIG
ID   ALBU_PIG       STANDARD;      PRT;   605 AA.
AC   P08835; [illegible]
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Serum albumin precursor (Fragment).
GN   ALB.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE [illegible]; PubMed=3174440;
RA   Baldwin [illegible], Weinstock [illegible];
RT   "Nucleotide sequence of porcine liver albumin.";
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RL   Nucleic Acids Res. 16:9045-9047(1988).
CC   -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
         BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
         BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
         COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X12422; CAA30970.1; -.
DR   EMBL; M36787; AAA36988.1; -.
DR   PIR; S01382; ABPGS.
DR   HSSP; P02768; 1E7H.
DR   InterPro; IPR000264; Serum albumin.
DR   Pfam; PF00273; Serum_albumin; 3.
DR   ProDom; PD002486; Serum albumin; 1.
DR   SMART; SM00103; ALBUMIN; 3.
DR   PROSITE; PS00212; ALBUMIN; 3.
KW   Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW   Copper.
FT   NON_TER       1      1
FT   SIGNAL       <1     16       BY SIMILARITY.
FT   PROPEP       17     22       BY SIMILARITY.
FT   CHAIN        23    605       SERUM ALBUMIN.
FT   DOMAIN       23    202       ALBUMIN 1.
FT   DOMAIN      209    394       ALBUMIN 2.
FT   DOMAIN      401    592       ALBUMIN 3.
FT   METAL        31     31       COPPER (BY SIMILARITY).
FT   DISULFID     75     84       BY SIMILARITY.
FT   DISULFID     97    113       BY SIMILARITY.
FT   DISULFID    112    123       BY SIMILARITY.
FT   DISULFID    145    190       BY SIMILARITY.
FT   DISULFID    189    198       BY SIMILARITY.
FT   DISULFID    221    267       BY SIMILARITY.
FT   DISULFID    266    274       BY SIMILARITY.
FT   DISULFID    286    300       BY SIMILARITY.
FT   DISULFID    299    310       BY SIMILARITY.
FT   DISULFID    337    382       BY SIMILARITY.
FT   DISULFID    381    390       BY SIMILARITY.
FT   DISULFID    413    459       BY SIMILARITY.
FT   DISULFID    458    469       BY SIMILARITY.
FT   DISULFID    482    498       BY SIMILARITY.
FT   DISULFID    497    508       BY SIMILARITY.
FT   DISULFID    535    580       BY SIMILARITY.
FT   DISULFID    579    588       BY SIMILARITY.
FT   CONFLICT    562    562       E -> D (IN REF. 1; AAA36988).
SQ   SEQUENCE   605 AA;  69418 MW;  4E556B0DD1AIE1FF CRC64;

  Query Match             77.7%;  Score 2411.5;  DB 1;  Length 605;
  Best Local Similarity   76.0%;  Pred. No. 3.3e-150;
  Matches  438;  Conservative   67;  Mismatches   70;  Indels    1;  Gaps    1;

Qy          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60
Db         23 DIYKS[illegible]
Qy         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
Db         83 NC[illegible]
Qy        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
Db        142 VALCADEFQEDEQKFWGKYLYEIARRHPYFYAPELLYYAIIYKDVFSECCQAAPKAACLLP 201
Qy        181 KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV[illegible]
Db        202 K[illegible]
Qy        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA [illegible]
Db        262 VHKE[illegible]
Qy        301 [illegible]
Db        322 [illegible]
Qy        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST [illegible]
Db        382 CAKE[illegible]
Qy        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVS[illegible]
Db        442 PTLVEVARKL[illegible]
Qy        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT [illegible]
Db        502 LVNRRP[illegible]
Qy        541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLV [illegible]
Db        562 [illegible]


RESULT 11
ALBU_MERUN
ID   ALBU_MERUN     STANDARD;      PRT;   [illegible] AA.
AC   O35090;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Serum albumin precursor.
GN   ALB.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MGS/Sea; TISSUE=Liver;
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Yoshida K., Sato-Ishihara A., [illegible];
RT   "Sequencing of cDNA encoding serum albumin and its extrahepatic
RT   synthesis in the Mongolian gerbil, Meriones unguiculatus.";
RL   DNA Res. 4:351-354(1997).
CC   -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC       BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC       BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC       COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: PLASMA.
CC   -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC   --------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
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CC   --------------------------------------------------------------------------
DR   EMBL; AB006187; BAA21765.1; -.
DR   HSSP; P02768; 1E7H.
DR   InterPro; IPR000264; Serum albumin.
DR   Pfam; PF00273; Serum_albumin; 3.
DR   PRINTS; PR00802; SERUMALBUMIN.
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DR   Prodom; PD002486; Serum_albumin; 1.
DR   SMART; SM00103; ALBUMIN; 3.
DR   PROSITE; PS00212; ALBUMIN, 3.
KW   Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW   Copper.
FT   SIGNAL        1     18       BY SIMILARITY.
FT   PROPEP       19     24       BY SIMILARITY.
FT   CHAIN        25    609       SERUM ALBUMIN.
FT   DOMAIN       25    206       ALBUMIN 1.
FT   DOMAIN      213    398       ALBUMIN 2.
FT   DOMAIN      405    596       ALBUMIN 3.
FT   METAL        28     28       COPPER.
FT   DISULFID     78     87       BY SIMILARITY.
FT   DISULFID    100    116       BY SIMILARITY.
FT   DISULFID    115    126       BY SIMILARITY.
FT   DISULFID    149    194       BY SIMILARITY.
FT   DISULFID    193    202       BY SIMILARITY.
FT   DISULFID    225    271       BY SIMILARITY.
FT   DISULFID    270    278       BY SIMILARITY.
FT   DISULFID    290    304       BY SIMILARITY.
FT   DISULFID    303    314       BY SIMILARITY.
FT   DISULFID    341    386       BY SIMILARITY.
FT   DISULFID    385    394       BY SIMILARITY.
FT   DISULFID    417    463       BY SIMILARITY.
FT   DISULFID    462    473       BY SIMILARITY.
FT   DISULFID    486    502       BY SIMILARITY.
FT   DISULFID    501    512       BY SIMILARITY.
FT   DISULFID    539    584       BY SIMILARITY.
FT   DISULFID    583    592       BY SIMILARITY.
SQ   SEQUENCE   609 AA;  68948 MW;  [illegible] CRC64;

  Query Match             76.9%;  Score 2387;  DB 1;  Length 609;
  Best Local Similarity   73.9%;  Pred. No. 1.3e-148;
  Matches  [illegible];  Conservative   65;  Mismatches  [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy          2 AHKSEVAHRFKDLGEENFKALVLIAFAQYL[illegible] 61
Db         27 AH[illegible] 86

Qy         62 CDKSLHTLFGDKLCTVATLRETYGEMADCCAK[illegible] 121
Db         87 CDKSLHTLFGDKLCSLPNECEKYAEMADCCAK[illegible] 146

Qy        122 VMCTAFHDNE[illegible] 181
Db        147 AM[illegible]TAF[illegible]ENA[illegible] 206

Qy        182 LDE[illegible] 241
Db        207 LDA[illegible] 266

Qy        242 HTE[illegible] 301
Db        267 [illegible] 326

Qy        302 LPSLAA[illegible]VE[illegible] 361
Db        327 LPALTADFVEDKEVCKNYAEAKDVFLG[illegible] 386

Qy        362 AAA[illegible] 421
Db        387 AHA[illegible] 446

Qy        422 [illegible] 481
Db        447 TLVEAARSL[illegible] 506

Qy        482 VNRRPCFSALEVDE[illegible] 541
Db        507 VEKKCFSA[illegible] 566

Qy        542 EQLKAVMD[illegible]AA[illegible]
Db        567 EQLKTVMDDFAQFLDTCCKAADKDTCFSTEGPNLVTRCKDALA 609
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RESULT 12
ALBU_MOUSE
ID   ALBU_MOUSE     STANDARD;      PRT;   608 AA.
AC   P07724; [illegible]
DT   01-APR-1988 (Rel. 07, Created)
DT   15-[illegible] (Rel. [illegible], Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Serum albumin precursor.
GN   ALB OR ALB1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C.;
RL   Submitted ([illegible]) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=[illegible];
RX   MEDLINE=21[illegible]; PubMed=[illegible];
RA   Kawai J., [illegible] M., [illegible] M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., [illegible]
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., [illegible] Y., [illegible] T., [illegible] H., Furukawa T., [illegible]
RA   Kanapin A., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., [illegible] T., [illegible], King B., [illegible]
RA   Kochl P., [illegible] S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., [illegible]
RA   [illegible] K., [illegible] H., Baldarelli R., Barsh G.,
RA   Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   [illegible], Garibaldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., [illegible]
RA   [illegible], Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., [illegible]
RA   Suzuki H., [illegible] K., Wang K.H., Weitz C., Whittaker C., [illegible]
RA   [illegible] H., [illegible]
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE [illegible] FROM N.A.
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Minghetti P.P., Law S.W., Dugaiczyk A.;
RT   "The rate of molecular evolution of alpha-fetoprotein [illegible]
RT   of pseudogenes.";
RL   Mol. [illegible](1985).
RN   [4]
RP   [illegible] FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=90269606; PubMed=[illegible];
RA   Boccaccio C., Deschatrette J., Meunier-Rotival M.;
RT   "Empty and occupied insertion site of the truncated LINE [illegible]
RT   located in the mouse serum albumin encoding gene.";
RL   Gene [illegible](1990).
RN   [5]
RP   SEQUENCE OF 2[illegible]-[illegible].
RC   TISSUE=Liver;
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Giometti C.S., Taylor J., [illegible] S.L.;
RT   "Mouse liver protein database: a catalog of proteins detected [illegible]
RT   dimensional gel electrophoresis.";
RL   Electrophoresis [illegible](1992).
CC   -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A [illegible]
CC       [illegible] WATER, [illegible], FATTY ACIDS, HORMONES,
CC       BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC       [illegible] PRESSURE OF BLOOD.
CC   -!- SUBCELLULAR LOCATION: Secreted.
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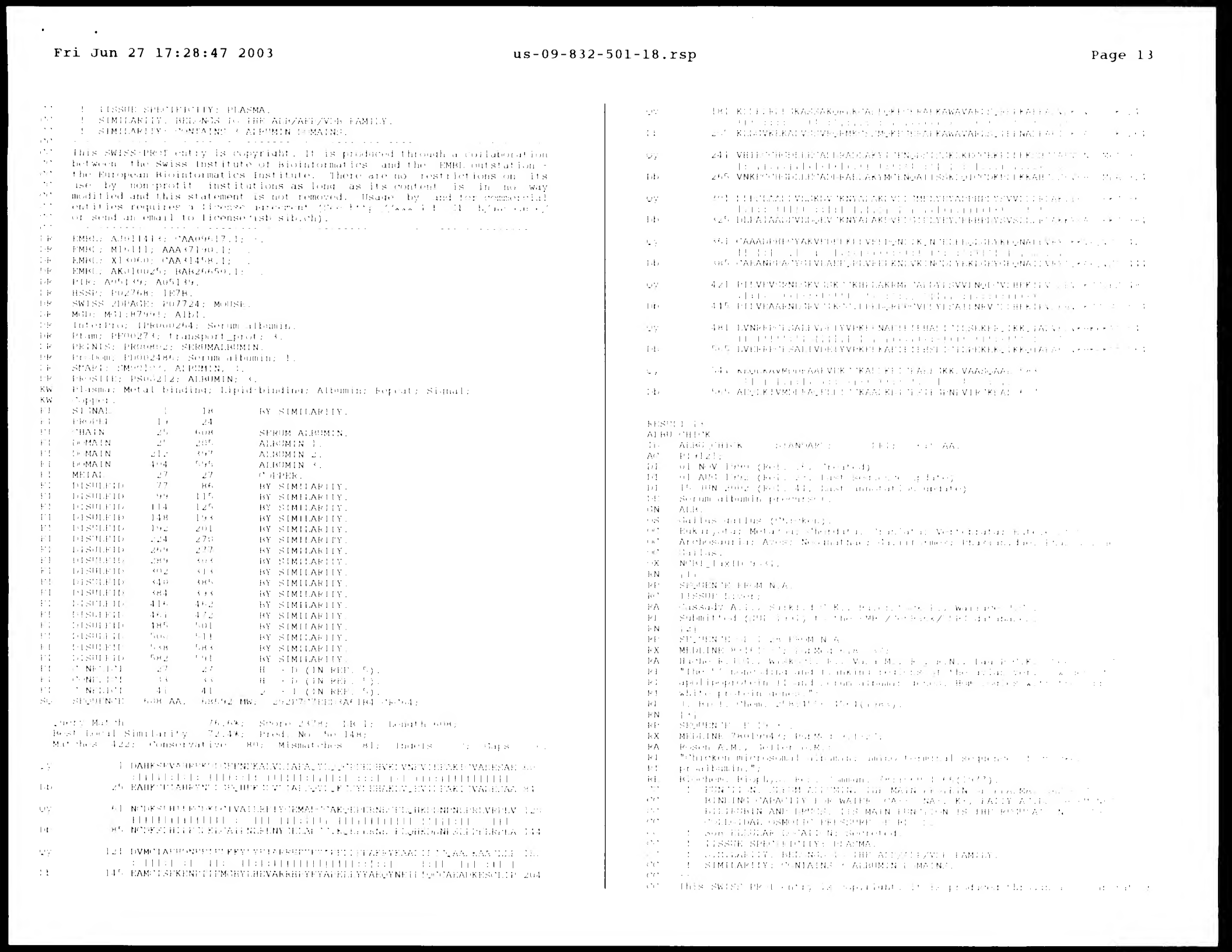

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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X60688; CAA43098.1; -.
DR   EMBL; V00181; CAA23630.1; -.
DR   PIR; S15571; ABCHS.
DR   HSSP; P02768; 1E7B.
DR   InterPro; IPR000264; Serum_albumin.
DR   Pfam; PF00273; transport_prot; 3.
DR   PRINTS; PR00802; SERUMALBUMIN.
DR   ProDom; PD002486; Serum_albumin; 1.
DR   SMART; SM00103; ALBUMIN; 3.
DR   PROSITE; PS00212; ALBUMIN; 3.
KW   Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW   Copper.
FT   SIGNAL        1     18
FT   PROPEP       19     23
FT   CHAIN        24    615       SERUM ALBUMIN.
FT   DOMAIN       24    209       ALBUMIN 1.
FT   DOMAIN      216    401       ALBUMIN 2.
FT   DOMAIN      408    599       ALBUMIN 3.
FT   METAL        30     30       COPPER (BY SIMILARITY).
FT   DISULFID     80     89       BY SIMILARITY.
FT   DISULFID    102    118       BY SIMILARITY.
FT   DISULFID    117    128       BY SIMILARITY.
FT   DISULFID    152    197       BY SIMILARITY.
FT   DISULFID    196    205       BY SIMILARITY.
FT   DISULFID    228    274       BY SIMILARITY.
FT   DISULFID    273    281       BY SIMILARITY.
FT   DISULFID    293    307       BY SIMILARITY.
FT   DISULFID    306    317       BY SIMILARITY.
FT   DISULFID    344    389       BY SIMILARITY.
FT   DISULFID    388    397       BY SIMILARITY.
FT   DISULFID    420    466       BY SIMILARITY.
FT   DISULFID    465    476       BY SIMILARITY.
FT   DISULFID    489    505       BY SIMILARITY.
FT   DISULFID    504    515       BY SIMILARITY.
FT   DISULFID    542    587       BY SIMILARITY.
FT   DISULFID    586    595       BY SIMILARITY.
FT   CARBOHYD    500    500       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     24     24       F -> M (IN REF. 3).
SQ   SEQUENCE   615 AA;  69918 MW;  E59E4BBCAB[illegible] [illegible];

  Query Match             50.2%;  Score 1557.5;  DB 1;  Length 615;
  Best Local Similarity   46.7%;  Pred. No. 1.6e-94;
  Matches  27[illegible];  Conservative  11[illegible];  Mismatches  1[illegible];  Indels  [illegible];  Gaps  [illegible];

Qy          3 HE[illegible]VA[illegible] 62
              [illegible]
Db         30 HK[illegible]AHRYNDLKEETFKAVAMITFAQYLQR[illegible] 89

Qy         63 DE[illegible]LHTLFGDKLCTVATLRETYGEMA[illegible] 121
              [illegible]
Db         90 SEPLPS[illegible]CQVEKPE[illegible]AMA[illegible] 14[illegible]

Qy        122 VMCTAFHDNEETFLKKYLYEIARRHP[illegible] 181
              [illegible]
Db        150 VICQEYQDNRVSFLGHFIYSVARRHPFLYAPAILSFAVDFEHALQSCCKESDVGACLDTK 209

Qy        182 [illegible]KA[illegible] 241
              [illegible]
Db        210 EIVMREKAKGVSVKQQ[illegible] 26[illegible]

Qy        242 HIECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPAD 30[illegible]
              [illegible]
Db        270 HKECCEKPMVEGMIDDMARMMSNLCSQQDVFSGKIKDCCEKPIVERSQCIMEAEFDEKPA 32[illegible]

Qy        302 LPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCC 3[illegible]
              [illegible]
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Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        422 LVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLV 4[illegible]
              [illegible]
Db        4[illegible]

Qy        482 NRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKE 5[illegible]
              [illegible]
Db        5[illegible] [illegible]

Qy        542 [illegible] 585
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Db        570 [illegible]VQSKATLGL[illegible] 61[illegible]


RESULT 14
FETA_PANTR
ID   FETA_PANTR     STANDARD;      PRT;   [illegible] AA.
AC   Q28780;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-
DE   fetoprotein).
GN   AFP.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   [illegible]
RT   "The chimpanzee alpha-fetoprotein-encoding gene shows structural
RT   similarity to that of gorilla but distinct differences from that of
RT   human.";
RL   Gene 162:213-220(1995).
CC   -!- [illegible] AS WELL AS [illegible]
CC       BILIRUBIN LESS WELL THAN SERUM ALBUMIN. ONLY A SMALL PERCENTAGE
CC       (LESS THAN 2%) OF THE HUMAN AFP SHOWS ESTROGEN BINDING PROPERTIES.
CC   -!- SUBUNIT: DIMERIC AND TRIMERIC FORMS HAVE BEEN FOUND IN ADDITION
CC       TO THE MONOMERIC FORM.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Plasma. Synthesized by the fetal liver and
CC       yolk sac.
CC   -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content is in no way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U21916; AAA[illegible].1; -.
DR   HSSP; P02768; 1E7B.
DR   InterPro; IPR000264; Serum_albumin.
DR   Pfam; PF00273; transport_prot; 3.
DR   PRINTS; PR00802; SERUMALBUMIN.
DR   ProDom; PD002486; Serum_albumin; 1.
DR   SMART; SM00103; ALBUMIN; 3.
DR   PROSITE; PS00212; ALBUMIN; 2.
KW   Glycoprotein; Sulfation; Albumin; Plasma; Repeat; Metal-binding;
KW   Copper; Nickel; Signal.
FT   SIGNAL        1     18       BY SIMILARITY.
FT   CHAIN        19    [illegible]       ALPHA-FETOPROTEIN.
FT   DOMAIN       20    20[illegible]       ALBUMIN 1.
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FT   DOMAIN      212    397       ALBUMIN 2.
FT   DOMAIN      404    595       ALBUMIN 3.
FT   METAL        22     22       COPPER AND NICKEL (BY SIMILARITY).
FT   DISULFID     99    114       BY SIMILARITY.
FT   DISULFID    113    124       BY SIMILARITY.
FT   DISULFID    148    193       BY SIMILARITY.
FT   DISULFID    192    201       BY SIMILARITY.
FT   DISULFID    224    270       BY SIMILARITY.
FT   DISULFID    269    277       BY SIMILARITY.
FT   DISULFID    289    303       BY SIMILARITY.
FT   DISULFID    302    313       BY SIMILARITY.
FT   DISULFID    384    [illegible]       BY SIMILARITY.
FT   DISULFID    41[illegible]    462       BY SIMILARITY.
FT   DISULFID    461    472       BY SIMILARITY.
FT   DISULFID    485    501       BY SIMILARITY.
FT   DISULFID    500    511       BY SIMILARITY.
FT   DISULFID    538    583       BY SIMILARITY.
FT   DISULFID    582    591       BY SIMILARITY.
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    251    251       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   [illegible] AA;  68741 MW;  [illegible]32987CAB0E67[illegible] [illegible]C064;

  Query Match             40.4%;  Score 1253.5;  DB [illegible];  Length [illegible];
  Best Local Similarity   40.1%;  Pred. No. 1.1e-74;
  Matches  23[illegible];  Conservative  11[illegible];  Mismatches  231;  Indels  [illegible];  Gaps  [illegible];

Qy          3 HKSP----VAHRFKDLGEENFKALVLIAFA[illegible]VNEVTEFAKTNVA[illegible] 5[illegible]

Db         22 HRNEYGIA[illegible]NI[illegible]A[illegible]V[illegible]AT[illegible]V[illegible]EMVK[illegible]A[illegible]A[illegible]KPIGDE 81

Qy         58 SAENCDKSLHTLFGDKLCTVATLRETYGEMAD[illegible]CAKQEPERNECFLQHKDDNP-NLPRLV 11[illegible]

Db         82 QSAC[illegible]LENQLEAFLEE[illegible]KEKE[illegible]LEKYGH[illegible]HRN[illegible]AR[illegible]PASIP[illegible] 14[illegible]

Qy        117 RPEV[illegible]VM[illegible]TAFHDNE[illegible]F[illegible]KKYLYE[illegible]ARRHPYFYAPELLFFAKRYKAAF[illegible]CCQAADKAA 176

Db        141 VPEPVTS[illegible]EAYEED[illegible]E[illegible]FMNKF[illegible]YEIARRHPFLYAP[illegible]WAARY[illegible]K[illegible]KAENAVE 200

Qy        177 CLLPKLDELRDEGKA[illegible]K[illegible]AK[illegible]LKC[illegible]SLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVT 2[illegible]

Db        [illegible]01 C[illegible]QTKAAIVIKEL[illegible]E[illegible]ASVMKNF[illegible]IPLA[illegible]IV[illegible]E[illegible]VNF[illegible]KLV[illegible] 2[illegible]

Qy        237 DLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVEND 296

Db        261 DVAHVHEHCCRGDVLDCLQDGEKIMSYI[illegible]SQ[illegible]LSNK[illegible]E[illegible]KL[illegible]LE[illegible]R[illegible]IHAENE 320

Qy        297 EMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETT 35[illegible]

Db        321 [illegible]ENF[illegible]A[illegible]V[illegible]HP[illegible]L[illegible]AV[illegible]VA[illegible]Y[illegible] [illegible]

Qy        357 LEK[illegible]CAAA[illegible]YAKV[illegible]VEE[illegible]L[illegible]N[illegible]NALLV[illegible]KKVP 416

Db        381 LEKCFQTENPLECQ[illegible]F[illegible]L[illegible]KTL[illegible]LA[illegible]ALARFS[illegible]KL[illegible]YTT[illegible]NZ[illegible]VA[illegible]KKAP 440

Qy        417 QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC 476

Db        441 QLTSSELMAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEETPVNPGVGQC 500

Qy        477 CTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHK 536

Db        501 CTSSYANRRPCFSSLVVDETYVPPAFSDDKFIFHKDLCQAQGVALQTMKQEFLINLVKQK 560

Qy        537 PKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585

Db        561 PQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGQKLISKTRAALGV 60[illegible]


RESULT 1[illegible]
FETA_HUMAN
ID   FETA_HUMAN     STANDARD;      PRT;   609 AA.
AC   P02771;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-
DE   fetoprotein)
GN   AFP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=8[illegible]; PubMed=[illegible];
RA   Morinaga T., Sakai M., Wegmann T.G., Tamaoki T.;
RT   "Primary structures of human alpha-fetoprotein and its mRNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. [illegible]:[illegible](198[illegible]).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Gibbs P.E.M., Zielinski R., [illegible] A.;
RT   "Structure, polymorphism, and novel repeated DNA elements [illegible]
RT   a complete sequence of the human alpha-fetoprotein gene.";
RL   Biochemistry [illegible]:[illegible](198[illegible]).
RN   [3]
RP   SEQUENCE OF [illegible] FROM N.A.
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   McVey J.H., Michaelides K., Hansen L.P., [illegible] Smith M.,
RA   Tilghman S., Krumlauf R., Tuddenham E.G.D.;
RT   "A G--&gt;A substitution in an HNF-1 binding site in the human alpha-
RT   fetoprotein gene is associated with hereditary persistence of alpha-
RT   fetoprotein (HPAFP).";
RL   Hum. Mol. Genet. 2:379-379(199[illegible]).
RN   [4]
RP   SEQUENCE OF 4[illegible]-[illegible] FROM N.A.
RX   MEDLINE=8315[illegible]; PubMed=[illegible];
RA   Beattie W.G., Dugaiczyk A.;
RT   "Structure and evolution of human alpha-fetoprotein deduced from a
RT   partial sequence of cloned cDNA.";
RL   Gene 20:415-422(1982).
RN   [5]
RP   PARTIAL SEQUENCE [illegible].
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Pucci P., Siciliano R., Malorni A., Marino G., [illegible] M.E.,
RA   Ceccarini C., Terrana B.;
RT   "Human alpha-fetoprotein primary structure: a mass spectrometric
RT   study.";
RL   Biochemistry [illegible]:[illegible](199[illegible]).
RN   [6]
RP   PRELIMINARY SEQUENCE OF [illegible].
RX   MEDLINE=7721[illegible]; PubMed=[illegible];
RA   Yachnin S., Hsu R., Heinrikson R.L., Miller J.B.;
RT   "Studies on human alpha-fetoprotein. Isolation and characterization
RT   of monomeric and polymeric forms and amino-terminal sequence
RT   analysis.";
RL   Biochim. Biophys. Acta 4[illegible]:[illegible]-[illegible](19[illegible]).
RN   [7]
RP   PRELIMINARY SEQUENCE OF [illegible].
RX   MEDLINE=78[illegible]; PubMed=[illegible];
RA   Aoyagi Y., Ikenaka T., Ichida F.;
RT   "Comparative chemical structures of human alpha-fetoproteins from
RT   fetal serum and from ascites fluid of a patient with hepatoma.";
RL   Cancer Res. [illegible]:[illegible](197[illegible]).
RN   [8]
RP   PRELIMINARY SEQUENCE OF [illegible].
RX   MEDLINE=75[illegible]; PubMed=[illegible];
RA   Ruoslahti E., Pihko H., Vaheri A., Seppala M., Virtanen I.,
RA   Kontiinen A.;
RT   "Alpha fetoprotein: structure and expression in man and inbred mouse
RT   strains under normal conditions and liver injury.";
RL   Johns Hopkins Med. J. Suppl. [illegible](19[illegible]).
RN   [9]
RP   GENE STRUCTURE.
RX   MEDLINE=8518[illegible]; PubMed=[illegible];
RA   Sakai M., Morinaga T., Urano Y., Watanabe K., Wegmann T.G.,
RA   Tamaoki T.;
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RT "The human alpha-fetoprotein gene. Sequence organization and the 5'
RT flanking region.";
RL J. Biol. Chem. 260:5055-5060(1985).
RN [10]
RP METAL BINDING.
RX MEDLINE=79001617; PubMed=80265;
RA Aoyagi Y., Ikenaka T., Ichida F.;
RT "Copper(II)-binding ability of human alpha-fetoprotein.";
RL Cancer Res. 38:3483-3486(1978).
RN [11]
RP BILIRUBIN-BINDING.
RX MEDLINE=80001710; PubMed=89903;
RA Aoyagi Y., Ikenaka T., Ichida F.;
RT "Alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-
RT binding ability.";
RL Cancer Res. 39:3571-3574(1979).
RN [12]
RP SULFATION.
RX MEDLINE=86042625; PubMed=2414772;
RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
RT "Tyrosine sulfation of proteins from the human hepatoma cell line
RT HepG2.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
CC -!- FUNCTION: BINDS COPPER, NICKEL, AND FATTY ACIDS AS WELL AS, AND
CC BILIRUBIN LESS WELL THAN, SERUM ALBUMIN. ONLY A SMALL PERCENTAGE
CC (LESS THAN 2%) OF THE HUMAN AFP SHOWS ESTROGEN BINDING PROPERTIES.
CC -!- SUBUNIT: DIMERIC AND TRIMERIC FORMS HAVE BEEN FOUND IN ADDITION
CC TO THE MONOMERIC FORM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLASMA. SYNTHESIZED BY THE FETAL LIVER AND
CC YOLK SAC.
CC -!- DEVELOPMENTAL STAGE: OCCURS IN THE PLASMA OF FETUSES OLDER THAN 1
CC WEEKS OLD, REACHES THE HIGHEST LEVELS DURING THE 12TH-16TH WEEK OF
CC GESTATION, AND DROPS TO TRACE AMOUNTS AFTER BIRTH. THE SERUM LEVEL
CC IN ADULTS IS USUALLY LESS THAN 40 NG/ML. AFP OCCURS ALSO AT HIGH
CC LEVELS IN THE PLASMA AND ASCITIC FLUID OF ADULTS WITH HEPATOMA.
CC -!- PTM: INDEPENDENT STUDIES SUGGEST HETEROGENEITY OF THE AMINO-
CC TERMINAL SEQUENCE OF THE MATURE PROTEIN AND OF THE CLEAVAGE SITE
CC OF THE SIGNAL SEQUENCE.
CC -!- PTM: SULFATED.
CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
CC --
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CC --
DR EMBL; M10949; AAA51674.1; -.
DR EMBL; M10950; AAA51675.1; -.
DR EMBL; V01514; CAA24759.1; -.
DR EMBL; M16110; AAB58754.1; -.
DR EMBL; Z19532; CAA79592.1; -.
DR PIR; A03234; FPHU.
DR PIR; A26624; A26624.
DR HSSP; P02768; 1E7B.
DR GlycoSuiteDB; P02771; -.
DR Siena-2DPAGE; P02771; -.
DR Genew; HGNC:317; AFP.
DR MIM; 104150; -.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 2.
KW Glycoprotein; Sulfation; Albumin; Plasma; Repeat; Metal binding;
KW Copper; Nickel; Signal; Polymorphism.
FT SIGNAL 1 18
FT CHAIN 19 609 ALPHA-FETOPROTEIN.
FT DOMAIN 20 205 ALBUMIN 1.
FT DOMAIN 212 397 ALBUMIN 2.
FT DOMAIN 404 593 ALBUMIN 3.
FT METAL 22 22 COPPER AND NICKEL.
FT DISULFID [illegible] 124
FT DISULFID 113 [illegible]
FT DISULFID [illegible] [illegible]
FT DISULFID 192 [illegible]
FT DISULFID 224 270
FT DISULFID 269 277
FT DISULFID 289 303
FT DISULFID 302 313
FT DISULFID 384 [illegible]
FT DISULFID 416 462
FT DISULFID 461 472
FT DISULFID 485 501
FT DISULFID 500 511
FT DISULFID 538 583
FT DISULFID 582 591
FT CARBOHYD 251 251 N-LINKED (GLCNAC . . .).
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FT /FTId=VAR_012049.
SQ [illegible]

Query Match [illegible]; Score [illegible]; DB 1; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 2[illegible]; Conservative [illegible]; Mismatches 231; Indels [illegible]

Qy [illegible]

Db 22 [illegible]

Qy [illegible]

Db [illegible]

Qy 117 [illegible]

Db 141 [illegible]

Qy [illegible]

Db 201 [illegible]

Qy [illegible]

Db 261 [illegible]

Qy [illegible]

Db 321 [illegible]

Qy [illegible]

Db [illegible]

Qy 417 [illegible]

Db [illegible]

Qy 477 [illegible]

Db 501 [illegible]

Qy 537 [illegible]

Db 561 [illegible]

Search completed: June 27, 2003, 17:12:[illegible]
Job time : 2[illegible] secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 27, 2003, 17:06:40 ; Search time 87 Seconds
(without alignments)
1385.189 Million cell updates/sec

Title: US-09-832-501-18
Perfect score: 3103
Sequence: 1 DAHKSEVA[illegible] .... [illegible]AKLVAA[illegible]AL[illegible] 585

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2504	80.7	608	5	Q95VB7	q95vb7 schistosoma
2	1242	40.0	626	13	Q8UW05	q8uw05 ambystoma m
3	1087	35.0	624	13	Q8UW06	q8uw06 ambystoma t
4	955	30.8	603	13	Q9YGH6	q9ygh6 rana shqipe
5	928.5	29.9	614	13	Q91134	q91134 naja naja (
6	713	23.0	417	11	Q8R0J9	q8r0j9 mus musculu
7	376.5	12.1	484	13	Q9W6F5	q9w6f5 gallus gall
8	373	12.0	476	11	Q9CY31	q9cy31 mus musculu
9	372	12.0	476	11	Q91X31	q91x31 mus musculu
10	365	11.8	551	13	O42279	o42279 petromyzon
11	331	10.7	122	13	Q90WZ8	q90wz8 larus argen
12	290	9.3	123	13	Q90WZ6	q90wz6 poephila gu
13	264	8.5	135	11	Q63205	q63205 rattus norv
14	188	6.1	1723	2	Q9JMX8	q9jmx8 helicobacte
15	184	5.9	1819	16	Q9ZLV0	q9zlv0 helicobacte
16	184	5.9	1927	16	O25262	o25262 helicobacte
17	162.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
18	162.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
19	161	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
20	156	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
21	154.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
22	153.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
23	151.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
24	150	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
25	149	4.8	[illegible]	[illegible]	[illegible]	[illegible]
26	148	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
27	142.5	4.6	[illegible]	[illegible]	[illegible]	[illegible]
28	141.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
29	138.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
30	138.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
31	137.5	4.4	[illegible]	[illegible]	[illegible]	[illegible]
32	135.5	4.4	[illegible]	[illegible]	[illegible]	[illegible]
33	134.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
34	134.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
35	134	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
36	134	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
37	132.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
38	131	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
39	128.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
40	128.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
41	128	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
42	128	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
43	128	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
44	126.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
45	126.5	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

ALIGNMENTS

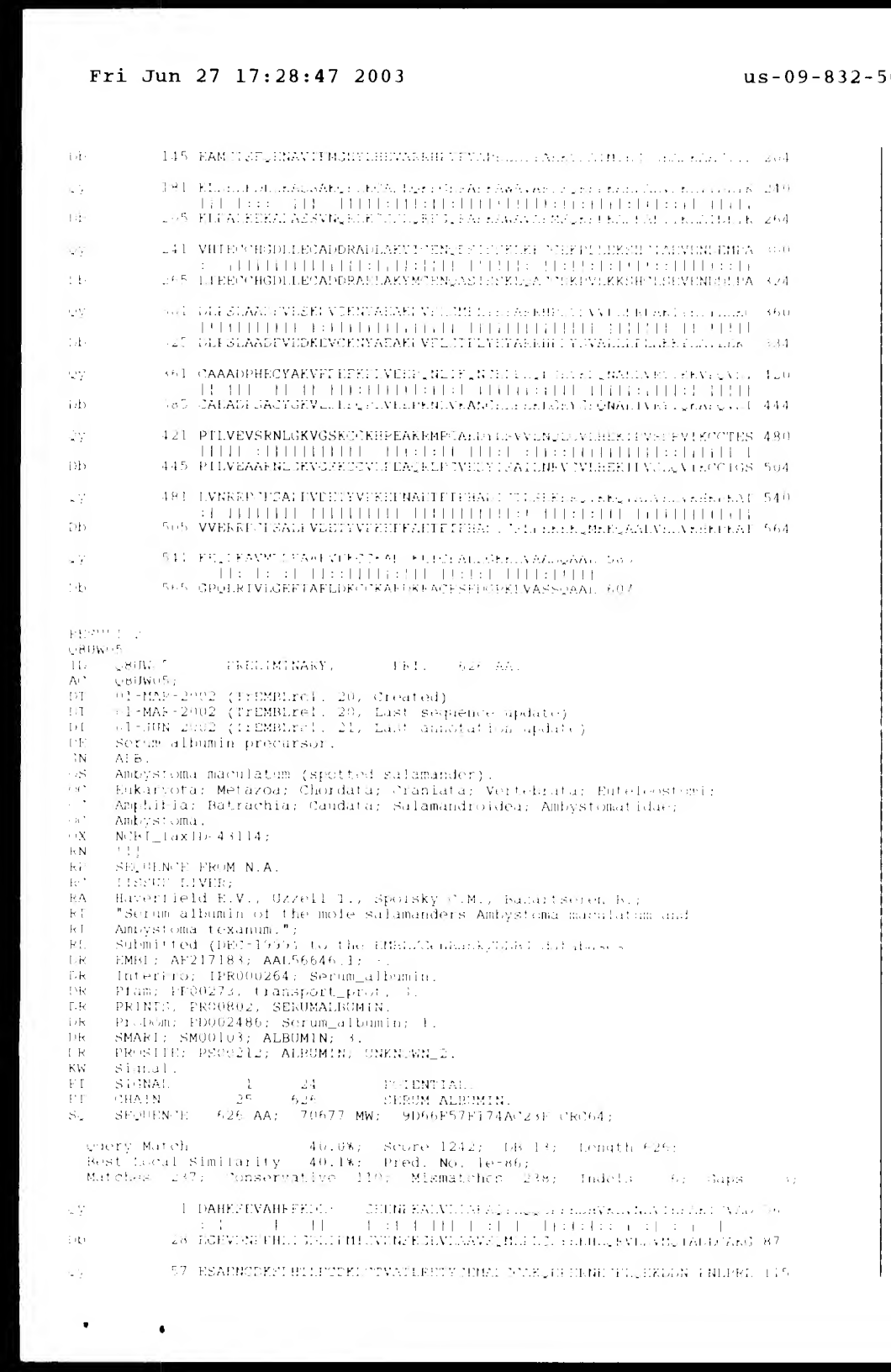
RESULT 1
Q95VB7
ID Q95VB7 PRELIMINARY; PRT; 608 AA.
AC Q95VB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. [illegible], Last annotation update)
DE Albumin.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; [illegible]
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RA Osman A., Asahi H., Stadecker M.J., LoVerde P.T.;
RT "Albumin precursor [illegible]
RT component in murine infection with Schistosoma mansoni.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF418[illegible]; AAL[illegible]
DR InterPro; IPR000264; Serum albumin.
DR Pfam; PF00273; Transport prot; [illegible]
DR ProDom; PD002[illegible]; Serum albumin; [illegible]
DR PROSITE; PS00212; ALBUMIN; UNKNOWN_[illegible]
SQ SEQUENCE 608 AA; [illegible] MW; [illegible] CRC64;

Query Match [illegible]; Score [illegible]; DB 5; Length 608;
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 445; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy 1 DAHKSEVAHRFKD[illegible]
Db 25 DAHKSEIAHRFKD[illegible]

Qy 61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHK[illegible]
Db 85 NCDKSLHTLFGDKLCTAT[illegible]

Qy 121 [illegible]



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Db        45 DIVEHAKALAMAESQMLSKCHHHEVQPVRNVHEIAEL [illegible] 1 4

Qy        74 [illegible] 1 2
             [illegible]
Db       165 [illegible] 1 4

Qy       1?? [illegible]
             [illegible]
Db       185 EELGHYIHEVA [illegible] 2 4

Qy       192 SSAKQELECASLQEFGERAFEAWAVARLSQ [illegible] 2 1
             [illegible]
Db       225 [illegible] 2 4

Qy       252 [illegible] 3 1
             [illegible]
Db       285 [illegible]

Qy       312 [illegible] 3 1
             [illegible]
Db       3?? [illegible]

Qy       372 [illegible]
             [illegible]
Db       397 [illegible] 45?

Qy       432 KV [illegible] 4 9
             [illegible]
Db       457 [illegible]

Qy       491 LEVSRTYVPKEFNAPTFTFHAD [illegible]
             [illegible]
Db       516 LIVDEIYVPAPVIAESFNFNDEF [illegible] 5 5

Qy       551 FAAFVEK [illegible] KAFECKEIVAA 579
             [illegible]
Db       576 FLAM [illegible] KA [illegible] FAIESAKLVEA [illegible]
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RESULT 4
Q9YGH6
ID   Q9YGH6      PRELIMINARY;      PRT;   603 AA.
AC   Q9YGH6;
DT   01 MAY 1999 (TrEMBLrel. 10, Created)
DT   01 MAY 1999 (TrEMBLrel. 10, Last sequence update)
DT   01 JUN 2002 (TrEMBLrel. 21, Last annotation update)
DE   Serum albumin precursor (Fragment).
GN   ALB.
OS   Rana shqiperica.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID 44326;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN BUSHAT; TISSUE LIVER;
RA   Uzzell T., Hotz H.;
RT   "Albumin cDNA sequence of Rana shqiperica: evolutionary changes in
RT   frog albumins.";
RL   Submitted (NOV 1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U40452; AAD09358.1; -.
DR   HSSP; P02768; 1E7B.
DR   InterPro; IPR000264; Serum_albumin.
DR   Pfam; PF00273; transport_prot; 3.
DR   PRINTS; PR00802; SERUMALBUMIN.
DR   ProDom; PD002486; Serum_albumin; 1.
DR   SMART; SM00103; ALBUMIN; 3.
DR   PROSITE; PS00212; ALBUMIN; 3.
KW   Signal.
FT   NON_TER       1      1
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    603       SERUM ALBUMIN.
SQ   SEQUENCE   603 AA;  69293 MW;  34913 [illegible] CRC64;
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Query Match [illegible]
Best Local Similarity [illegible]
Matches [illegible] Conservative [illegible] Mismatches [illegible]

Qy        12 [illegible]
             [illegible]
Db         ? [illegible]

Qy        72 [illegible]
             [illegible]
Db         9? [illegible]

Qy       126 [illegible]
             [illegible]
Db       1?? [illegible]

Qy       186 [illegible]
             [illegible]
Db       209 [illegible]

Qy       2?6 [illegible]
             [illegible]
Db       269 [illegible]

Qy       ??? [illegible]
             [illegible]
Db       327 [illegible]

Qy       ??? [illegible]
             [illegible]
Db       3?? [illegible]

Qy       42? [illegible]
             [illegible]
Db       447 [illegible]

Qy       486 [illegible]
             [illegible]
Db       507 [illegible]

Qy       546 AVMDDFAAEVEK [illegible] KADEKE [illegible] ALE [illegible]
             [illegible]
Db       567 EVIE [illegible] EKIVVE [illegible] AALN [illegible] LE [illegible]
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RESULT 5
Q91134
ID   Q91134      PRELIMINARY;      PRT;   [illegible] AA.
AC   Q91134;
DT   01 NOV 1996 (TrEMBLrel. [illegible], Created)
DT   01 NOV 1996 (TrEMBLrel. [illegible], Last sequence update)
DT   01 JUN 2002 (TrEMBLrel. [illegible], Last annotation update)
DE   Cobra serum albumin.
OS   Naja naja (Indian cobra).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
OC   Lepidosauria; Squamata; [illegible] Serpentes; [illegible]
OC   Elapidae; Elapinae; Naja.
OX   NCBI_TaxID [illegible];
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE LIVER;
RX   MEDLINE [illegible]; PubMed [illegible];
RA   Wang X., Hansen H., Bergsteen B.;
RT   "Evidence of the [illegible] and its [illegible]
RT   antitoxin. Cloning, sequence and expression of a serum albumin [illegible]
RT   the chinese cobra.";
RL   [illegible]
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE LIVER;
RX   MEDLINE [illegible]; PubMed [illegible];
RA   [illegible], Shen H., [illegible] B.;
RT   "Purification, characterization, and [illegible]
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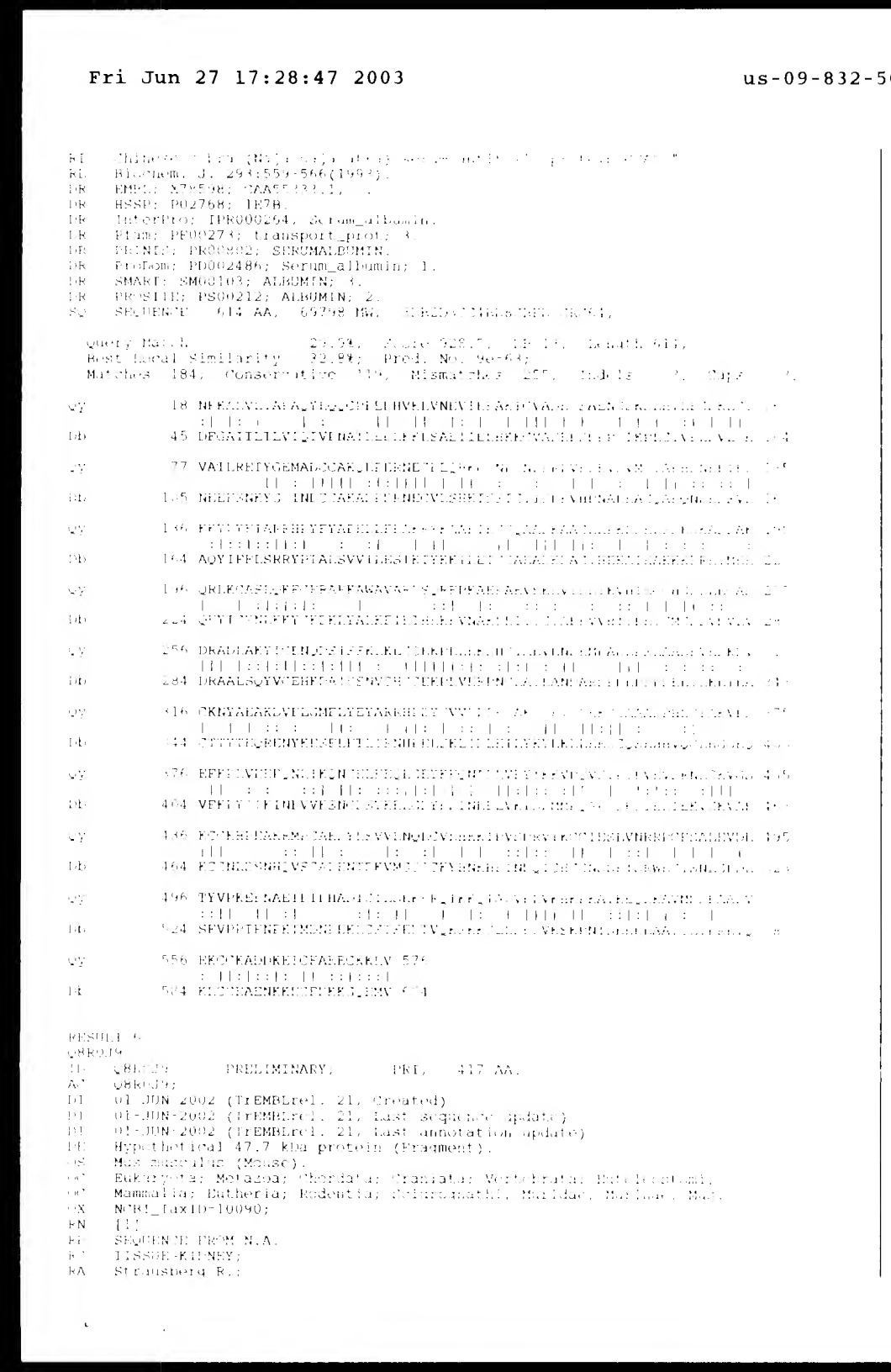
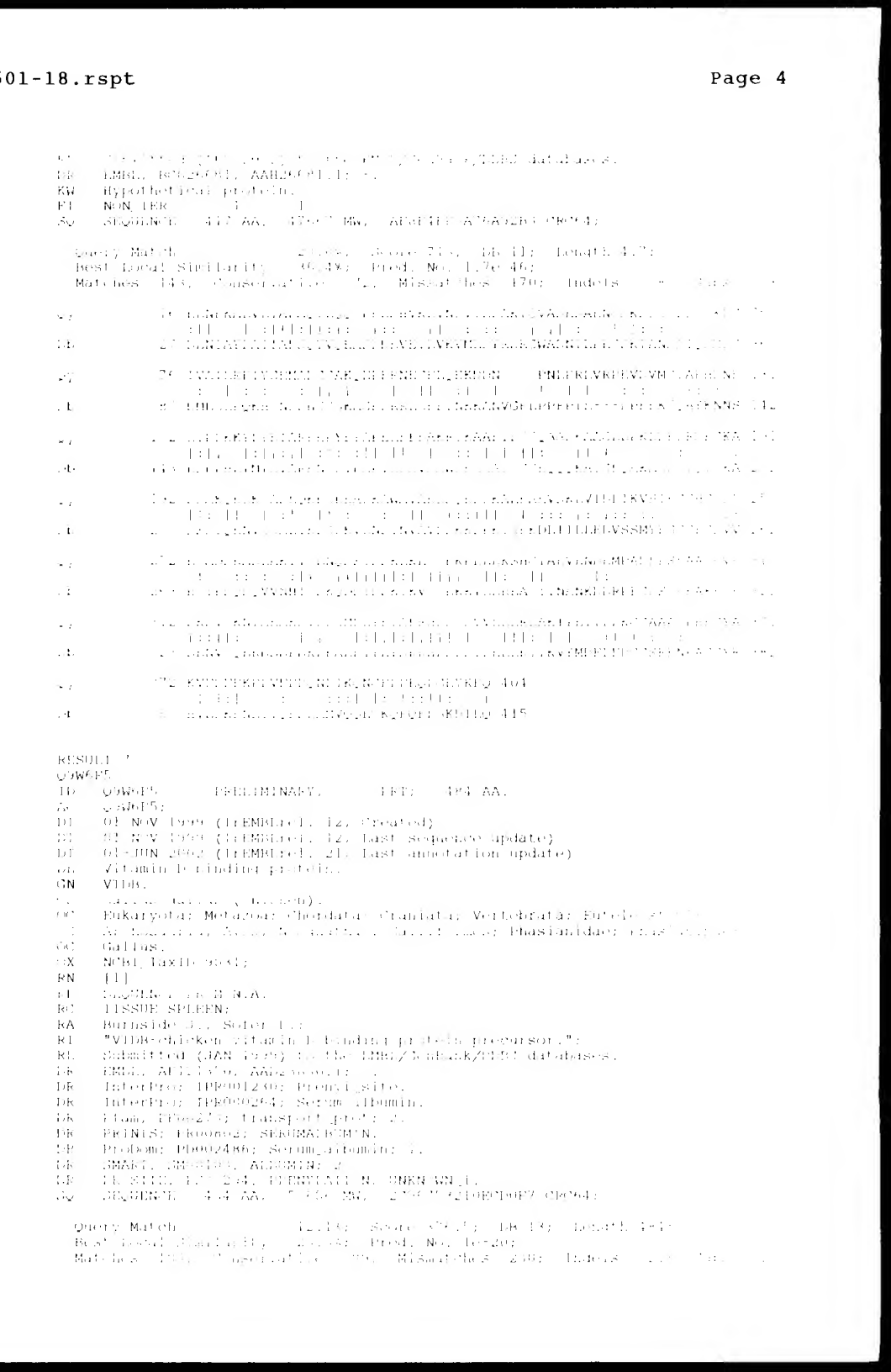


RESULT 5
Q8R0J9
ID Q8R0J9 PRELIMINARY; PRT; 417 AA.
AC Q8R0J9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 47.7 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;



RESULT 6
Q9W0F5
ID Q9W0F5 PRELIMINARY; PRT; 194 AA.
AC Q9W0F5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vitamin D-binding protein.
GN VDB.
OS [illegible] (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Burnside J., Soter L.;
RT "VDB=chicken vitamin D binding protein precursor.";
RL Submitted (JAN 1999) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF[illegible]; AAD[illegible]; -.
DR InterPro; IPR001230; Prion_gsite.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 2.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 2.
DR PROSITE; PS00212; ALBUMIN; 2.
SQ SEQUENCE 417 AA; 47[illegible] MW; [illegible] CRC64;

Query Match [illegible]; Score 213; DB 13; Length 417;
Best Local Similarity 46.4%; Pred. No. 1.7e-46;
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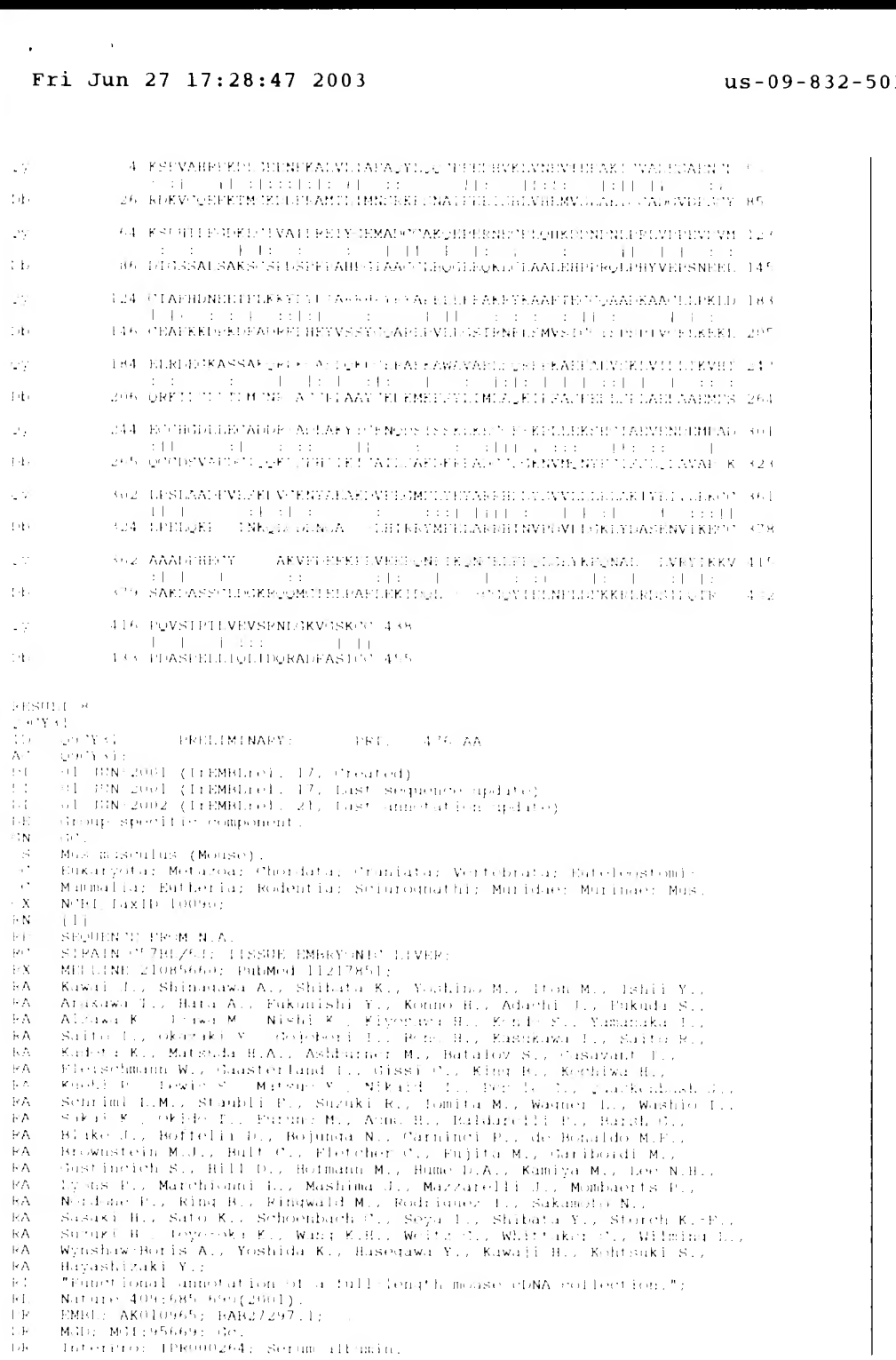
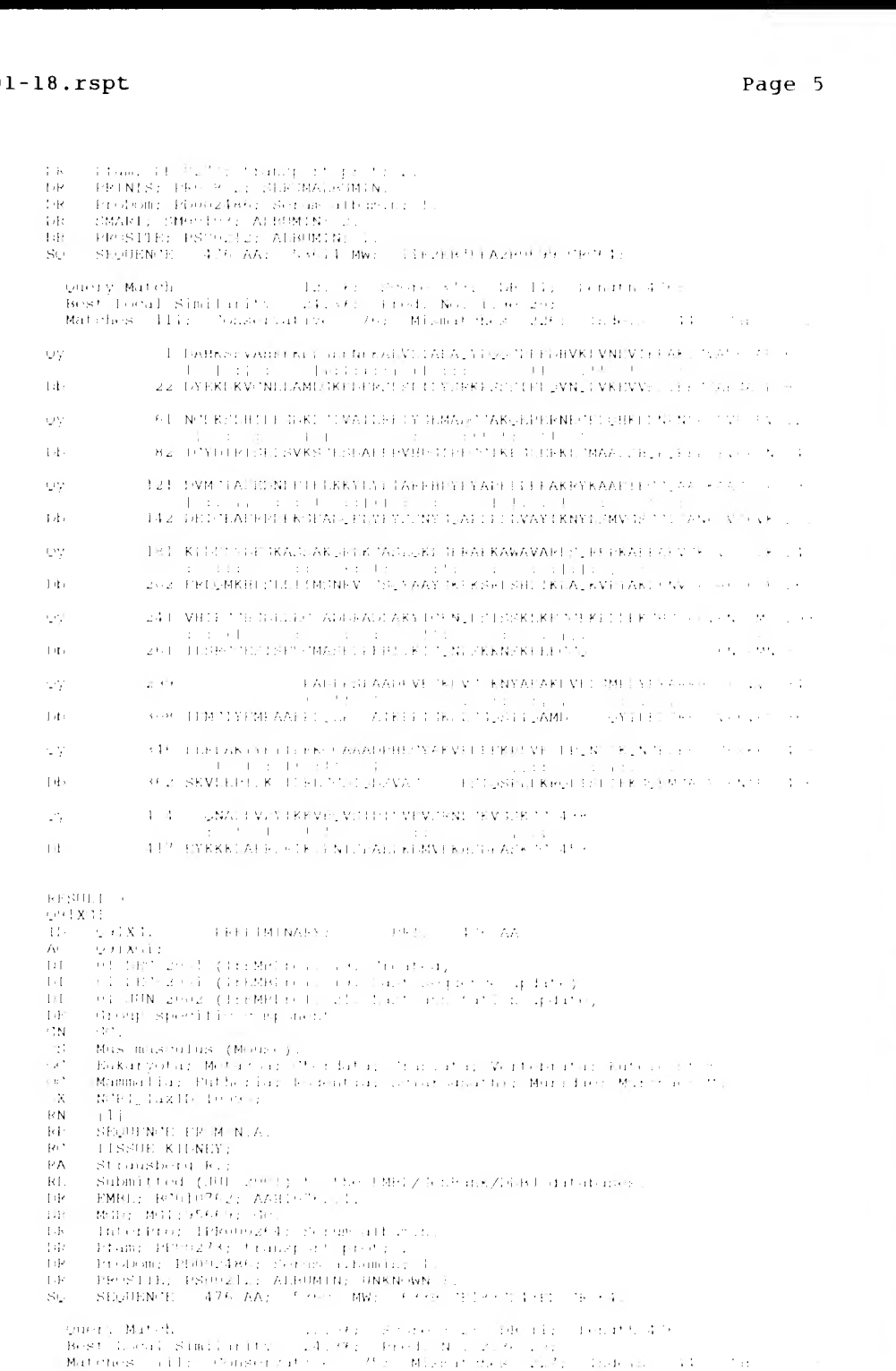


RESULT 8
Q96Y41
ID Q96Y41 PRELIMINARY; PRT; 476 AA.
AC Q96Y41;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Group specific component.
GN Gc.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kouda P., Lewis S., Letovsky S., Makalowski W., Moore J.,
RA Nehrini L.M., Stanbli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyoda K., Wada K.H., Wall C., Wells C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010965; BAB27297.1;
DR MGD; MGI:95669; Gc.
DR InterPro; IPR000264; Serum_albumin.



RESULT 9
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ID Q96IX3 PRELIMINARY; PRT; 476 AA.
AC Q96IX3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Group specific component.
GN Gc.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC010762; AAH10762.1;
DR MGD; MGI:95669; Gc.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; Transport_protein.
DR ProDom; PD001480; Serum_albumin; 1.
DR PROSITE; PS00071; ALBUMIN; UNKNOWN_1.
SQ SEQUENCE 476 AA; MW;

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Qy          1 DAHK[illegible]TVAHRFKD[illegible] [illegible]
Db         22 [illegible] [illegible]

Qy         61 N[illegible]DK[illegible] [illegible]TVATLRETYGEMA[illegible]CAKQE[illegible] [illegible]VKEPEV 120
Db         82 TCYDIRISELSVKSCESDA[illegible]PVHEGTPE[illegible]KEGLERK[illegible]MAALSHQ[illegible]N 141

Qy        121 DVMCTAF[illegible]NEETFLKKYLYEIA[illegible] [illegible]
Db        142 DEICEAFRKD[illegible] [illegible] 201

Qy        1[illegible] E[illegible]LLF[illegible]E[illegible]AKQ[illegible] [illegible]
Db        202 EKLQMFHL[illegible]TTRSNFV[illegible]YAAYGKPE[illegible] [illegible]

Qy        241 VHTECCHGDLLEC-ADDKADLAK[illegible] [illegible]
Db        2[illegible] ILSRCCESTSEDCMASEL[illegible] [illegible]

Qy        299 ------------PADLPSLAAE[illegible]VESKDV[illegible]KNYAEAK[illegible] [illegible]
Db        [illegible] [illegible]AAEFL[illegible] [illegible]

Qy        [illegible] LLRLAK[illegible]YETTLEK[illegible]CAAA[illegible] [illegible]
Db        3[illegible]2 SEVLEPTLE[illegible]TLA[illegible] [illegible]

Qy        404 --QNALLVRYTKKVP[illegible]V[illegible] [illegible]
Db        417 EYKKELA[illegible]ELETEIPN[illegible] [illegible]
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RESULT 10
O42279
ID   O42279   PRELIMINARY;   PRT;   551 AA.
AC   O42279;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Serum albumin AS (Fragment).
GN   AS.
OS   Petromyzon marinus (Sea lamprey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC   Petromyzontiformes; Petromyzontidae; Petromyzon.
OX   NCBI_TaxID=7757;
RN   [1]
RP   SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
RC   TISSUE=LARVAL LIVER;
RX   MEDLINE=98428063; PubMed=9755481;
RA   Filosa M.F., Adam [illegible], [illegible]
RA   Youson J.H.;
RT   "Partial [illegible] of the [illegible] for AS protein [illegible] lamprey, [illegible]
RT   marinus, a member of the albumin supergene family whose expression is
RT   restricted to the larval and metamorphic phases of the life cycle.";
RL   J. Exp. Zool. 282:301-309(1998).
RN   [2]
RP   DEVELOPMENTAL STAGE.
RX   PubMed=10998585;
RA   Danis M.B., Filosa M.F., Youson J.H.;
RT   "An albumin like protein in the serum of non parasitic brook lamprey
RT   (Lampetra appendix) is restricted to preadult phases of the life cycle
RT   in contrast to the parasitic species Petromyzon marinus.";
RL   Comp. Biochem. Physiol. 127B:251-260(2000).
CC   -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A [illegible]
CC   BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC   BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC   COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC   -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC   -!- DEVELOPMENTAL STAGE: LARVAL (AMMOCOETE), METAMORPHOSING, AND
CC   JUVENILE INDIVIDUALS, BUT NOT IN SEXUALLY MATURE ADULTS.
CC   -!- DOMAIN: COMPOSED OF AT LEAST THREE HOMOLOGOUS DOMAINS.
CC   -!- MISCELLANEOUS: IN THE SEA LAMPREY, THERE ARE TWO FORMS [illegible]
CC   AS AND SDS-1.
CC   -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
DR   EMBL; [illegible]; AAC[illegible];
DR   InterPro; IPR000264; Serum_albumin.
DR   Pfam; PF00273; transport [illegible]
DR   PRINTS; PR00802; SERUMALBUMIN.
DR   ProDom; PD002186; Serum albumin; 2.
DR   SMART; SM00103; ALBUMIN; 2.
DR   [illegible]
KW   Plasma; Metal binding; Lipid binding; Albumin; Repeat; [illegible]
FT   NON_TER   1   1
FT   CHAIN   1   551   SERUM ALBUMIN AS.
FT   [illegible]
FT   REPEAT   [illegible]   127   1.
FT   REPEAT   11[illegible]   3[illegible]   2.
FT   REPEAT   3[illegible]   5[illegible]   3.
FT   [illegible]   BY SIMILARITY.
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FT   [illegible]   BY SIMILARITY.
FT   DISULFID   [illegible]   11[illegible]   BY SIMILARITY.
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FT   DISULFID   149   1[illegible]   BY SIMILARITY.
FT   [illegible]   BY SIMILARITY.
FT   DISULFID   21[illegible]   23[illegible]   BY SIMILARITY.
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FT   DISULFID   344   3[illegible]   BY SIMILARITY.
FT   [illegible]   BY SIMILARITY.
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FT   [illegible]   BY SIMILARITY.
FT   DISULFID   48[illegible]   5[illegible]   BY SIMILARITY.
FT   DISULFID   53[illegible]   5[illegible]   BY SIMILARITY.
FT   CARBOHYD   58   58   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   174   174   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   [illegible]   [illegible]   N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   551 AA; [illegible] MW; 2A[illegible]244E555 CRC64;

  Query Match   [illegible]; Score [illegible]; DB 1[illegible]; Length [illegible];
  Best Local Similarity   2[illegible]; Pred. No. [illegible] 20;
  Matches 134; Conservative [illegible]; Mismatches 264; Indels [illegible]; Gaps [illegible];

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Qy        [illegible]
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Qy        [illegible]
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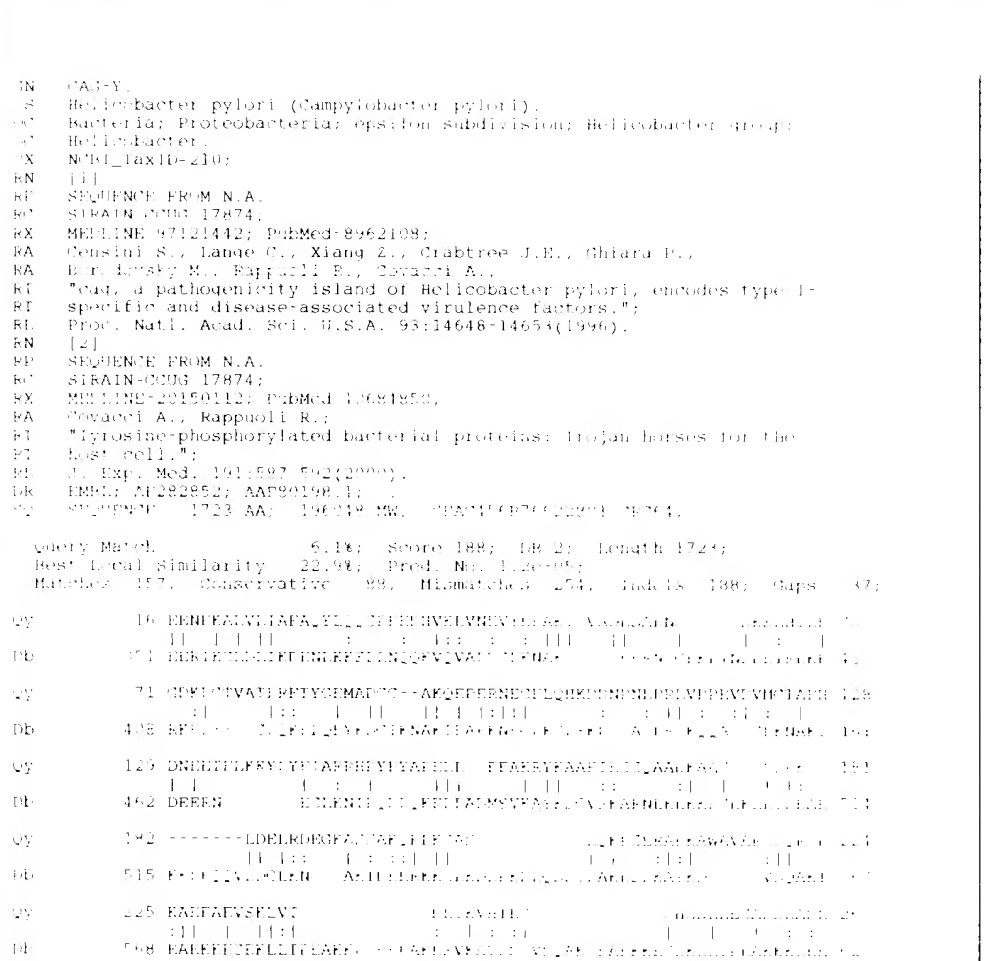

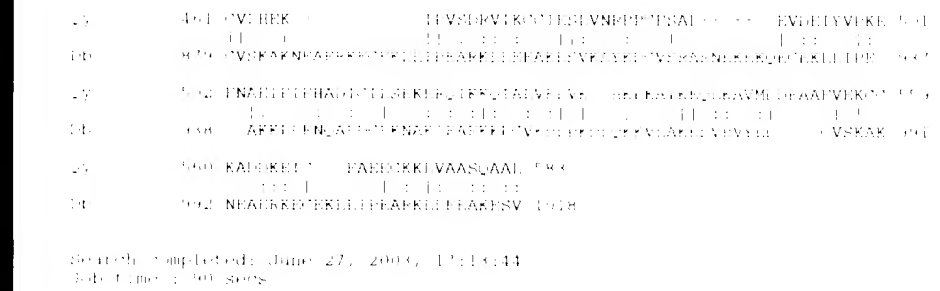

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Job Time : 700 secs

GenCore version 5.1.[illegible]

OM protein - protein search, using sw model

Run on: June 27, 2003, 17:10:26 ; Search time 27 Seconds
(without alignments)
[illegible] Million cell updates/sec

Title: US-09-832-501-18
Perfect score: 3103
Sequence: 1 LAHFSEVAHRFKDL[illegible]...... [illegible] 585

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 20422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: [illegible]*
3: [illegible]*
4: [illegible]*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3103	100.0	585	1	US-08-153-799-14	Sequence 14, Appl
2	3103	100.0	585	2	US-08-702-552-2	Sequence 2, Appli
3	3103	100.0	585	4	US-08-769-245-2	Sequence 2, Appli
4	3103	100.0	619	2	US-08-797-689-2	Sequence 2, Appli
5	3103	100.0	783	1	US-08-256-908-2	Sequence 2, Appli
6	3103	100.0	787	1	US-08-256-908-4	Sequence 4, Appli
7	3103	100.0	787	2	US-08-747-684-16	Sequence 16, Appl
8	[illegible]	99.9	609	1	US-08-222-619-3	Sequence 3, Appli
9	[illegible]	99.9	609	1	US-08-433-037-4	Sequence 4, Appli
10	[illegible]	99.9	609	4	US-08-897-[illegible]A-2	Sequence 2, Appli
11	[illegible]	99.9	609	5	PCT-US95-04075-3	Sequence 3, Appli
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15	2458.5	79.2	583	1	US-08-448-196A-5	Sequence 5, Appli
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20	1249.5	40.3	609	1	US-08-222-619-4	Sequence 4, Appli
21	1249.5	40.3	609	5	PCT-US95-04075-4	Sequence 4, Appli
22	1209.5	38.9	590	2	US-08-477-399-2	Sequence 2, Appli
23	1209.5	38.9	590	4	US-09-186-723-2	Sequence 2, Appli
24	1209.5	38.9	590	4	US-08-[illegible]-5	Sequence 5, Appli
25	1209.5	38.9	590	4	US-09-186-[illegible]A-3	Sequence 3, Appli
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45	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	Sequence [illegible]

ALIGNMENTS

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; Sequence 14, Application US/08153799
; Patent No. [illegible]
; GENERAL INFORMATION:
; APPLICANT: [illegible]
; APPLICANT: [illegible]
; TITLE OF INVENTION: [illegible]
; NUMBER OF SEQUENCES: [illegible]
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: [illegible]
; STREET: [illegible]
; CITY: [illegible]
; STATE: New Jersey
; COUNTRY: USA
; ZIP: [illegible]
; COMPUTER READABLE FORM:
; MEDIUM TYPE: [illegible]
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,799
; FILING DATE:
; CLASSIFICATION: [illegible]
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: [illegible]
; FILING DATE: [illegible]
; PRIOR APPLICATION DATA:
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; FILING DATE: [illegible]
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: [illegible]
; FILING DATE: [illegible]
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: [illegible]
; FILING DATE: [illegible]
; ATTORNEY/AGENT INFORMATION:
; NAME: [illegible]
; REGISTRATION NUMBER: [illegible]
; REFERENCE/DOCKET NUMBER: [illegible]
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: [illegible]
; TELEFAX: [illegible]
; TELEX: [illegible]
; INFORMATION FOR SEQ ID NO: [illegible]
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;     FEATURE:
;       NAME/KEY:  Region
;       LOCATION:  369..419
;       OTHER INFORMATION:  /note= "Alternative C terminal tail
;       OTHER INFORMATION:  HSA(1-n)"
;     FEATURE:
;       NAME/KEY:  Region
;       LOCATION:  1..585
;       OTHER INFORMATION:  /note= "Amino acid sequence of
;       OTHER INFORMATION:  natural HSA"
US-08-832-501-18

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  Best Local Similarity   100.0%;  Pred. No. 0.0e+000;
  Matches  585;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE  60

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Qy        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC  360
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Qy        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST  420
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Qy        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT  540
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RESULT 2
US-08-832-501-2
; Sequence 2, Application US/08832501
; Patent No. 5965386
; GENERAL INFORMATION:
;     APPLICANT:  Kerry-Williams, Sean M
;     APPLICANT:  Gilbert, Sarah C
;     TITLE OF INVENTION:  Yeast Strains and Modified Albumins
;     NUMBER OF SEQUENCES:  16
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Centeon L.L.C.
;       STREET:  1020 First Avenue
;       CITY:  King of Prussia
;       STATE:  Pennsylvania
;       COUNTRY:  USA
;       ZIP:  19406-1410
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  MicroSoft Word 6.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/832,501
;       FILING DATE:  11-APR-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO 96/28562
;       FILING DATE:  14-MAR-1996
;       APPLICATION NUMBER:  GB 9505701.2
;       FILING DATE:  16-MAR-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Naomi Biswas
;       REGISTRATION NUMBER:  35,891
;       REFERENCE/DOCKET NUMBER:  CEO-014 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  610/878-4264
;       TELEFAX:  610/878-4252
;     INFORMATION FOR SEQ ID NO:  2:
;       SEQUENCE CHARACTERISTICS:
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;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-832-501-2

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Qy         61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV  120
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Qy        121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP  180
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Qy        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA  300

Qy        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC  360
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Qy        361 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST  420
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Qy        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES  480
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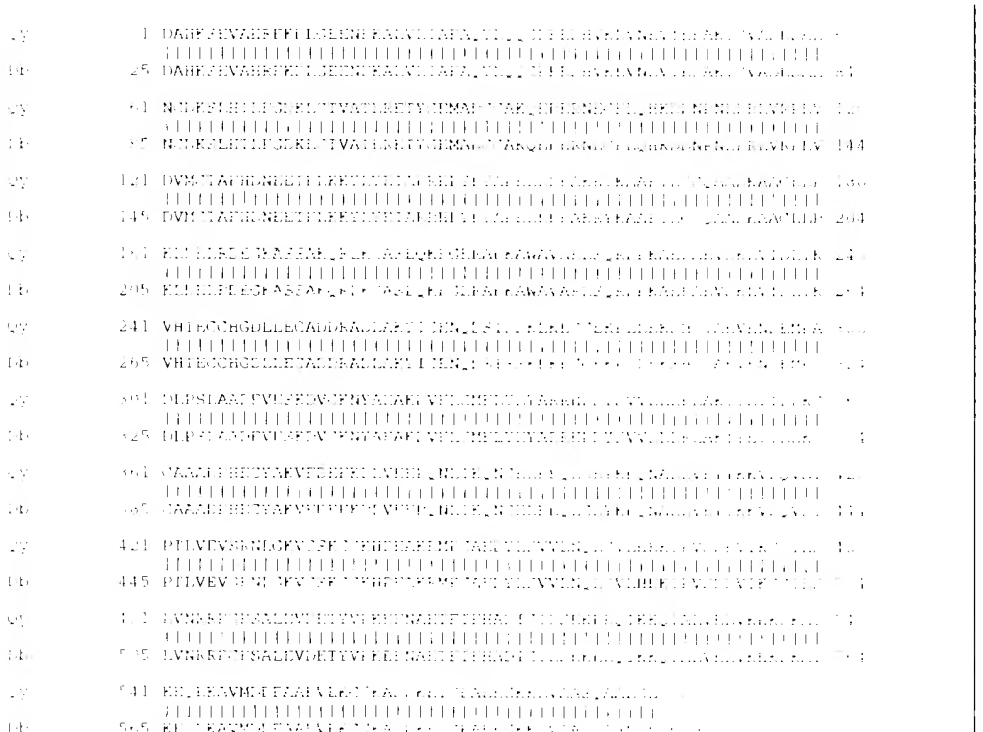

RESULT 5
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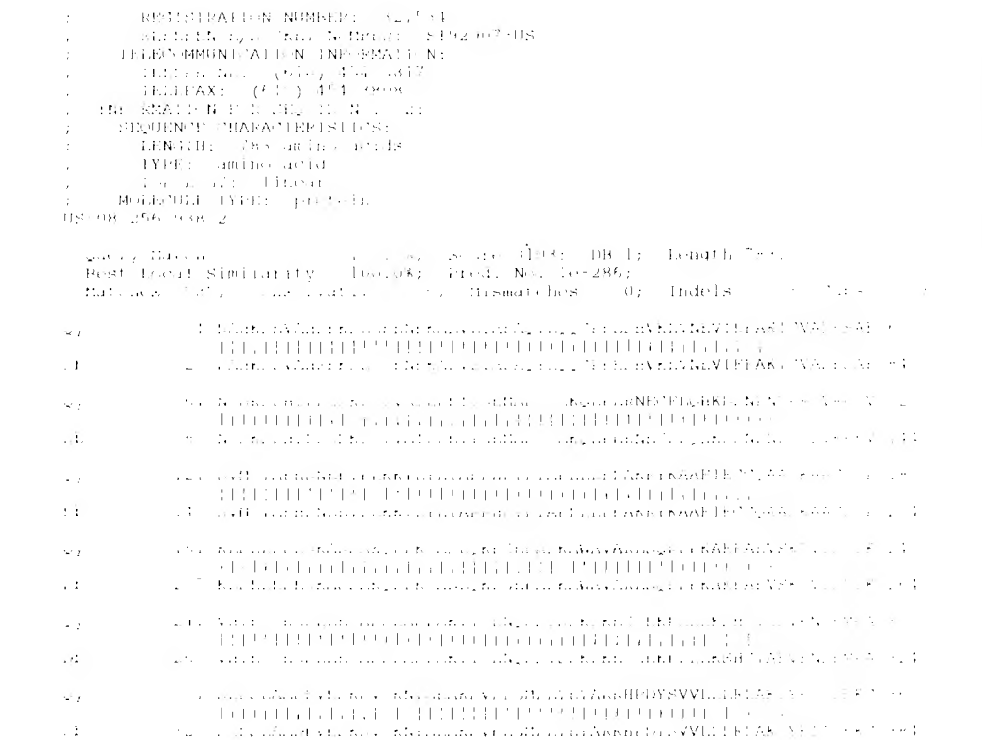
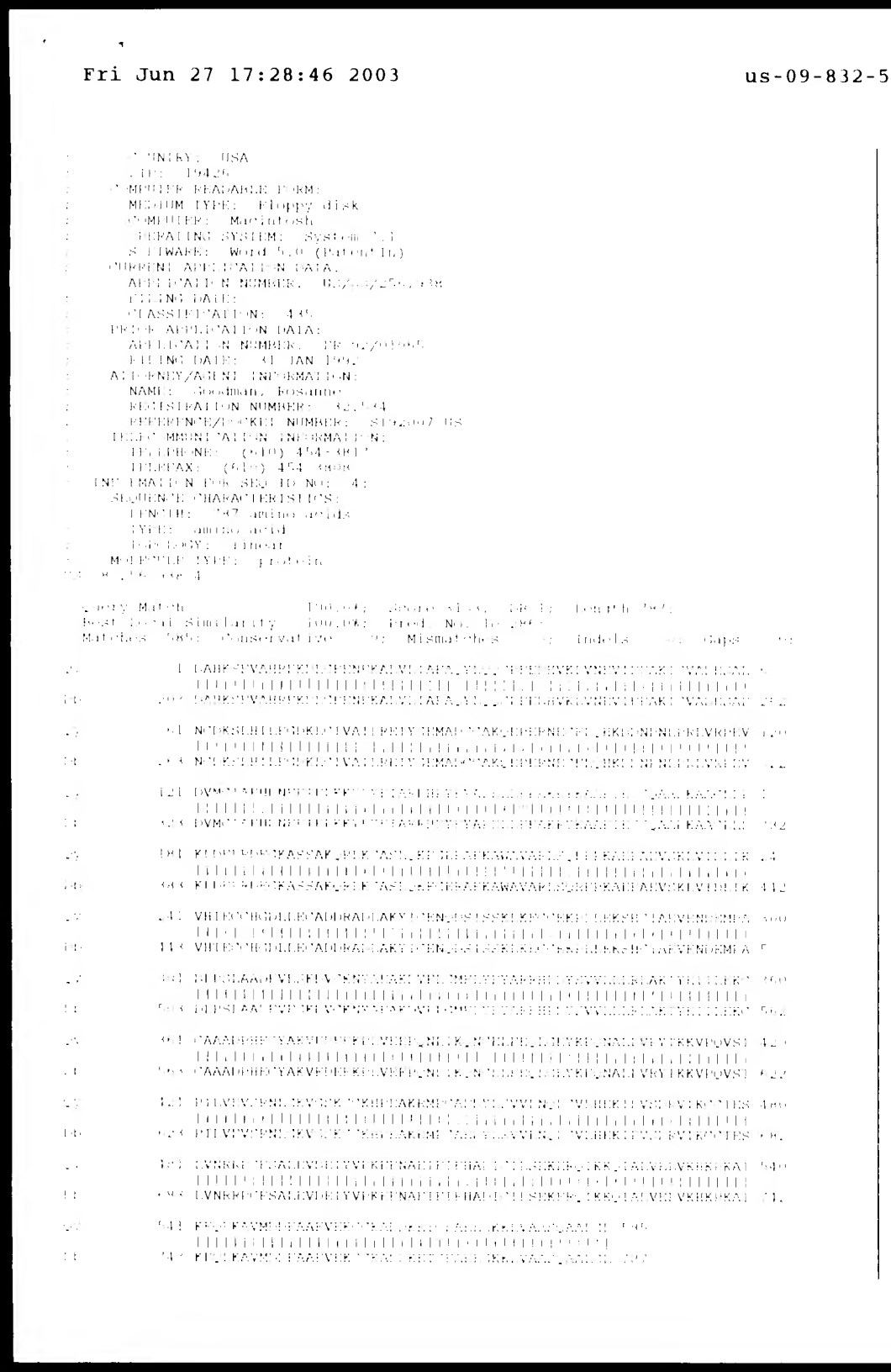
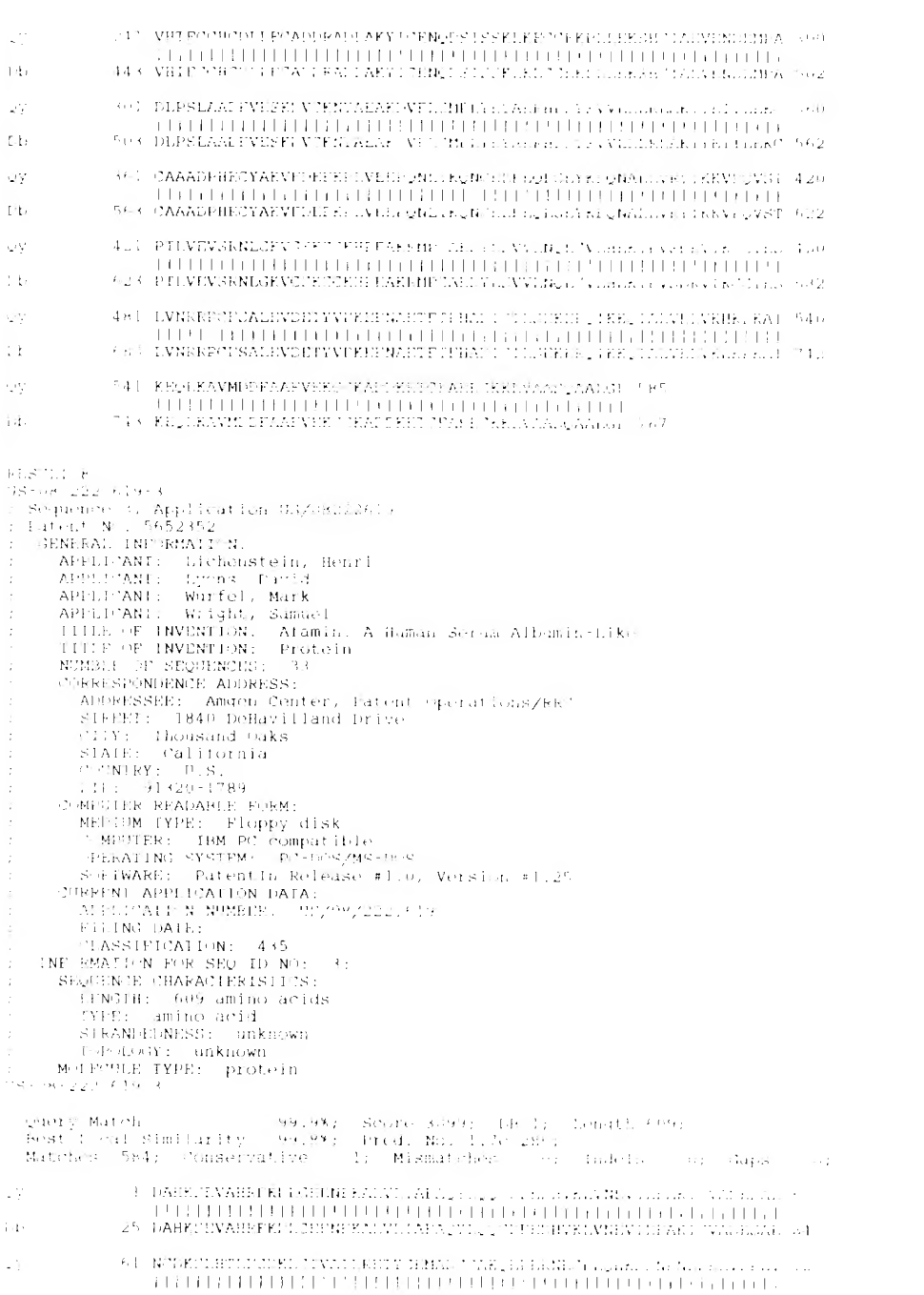
; Patent No. 5665862
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AN
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone Poulenc Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne



RESULT 6
US-08-256-938-4
; Sequence 4, Application US/08256938
; Patent No. 5665862
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AN
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA





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US-08-433-037-4
; Sequence 4, Application US/08433037
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Würfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Atamin, A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,037
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-433-037-4

Query Match 99.8%; Score 3294; DB 1; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.3e-285;
Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
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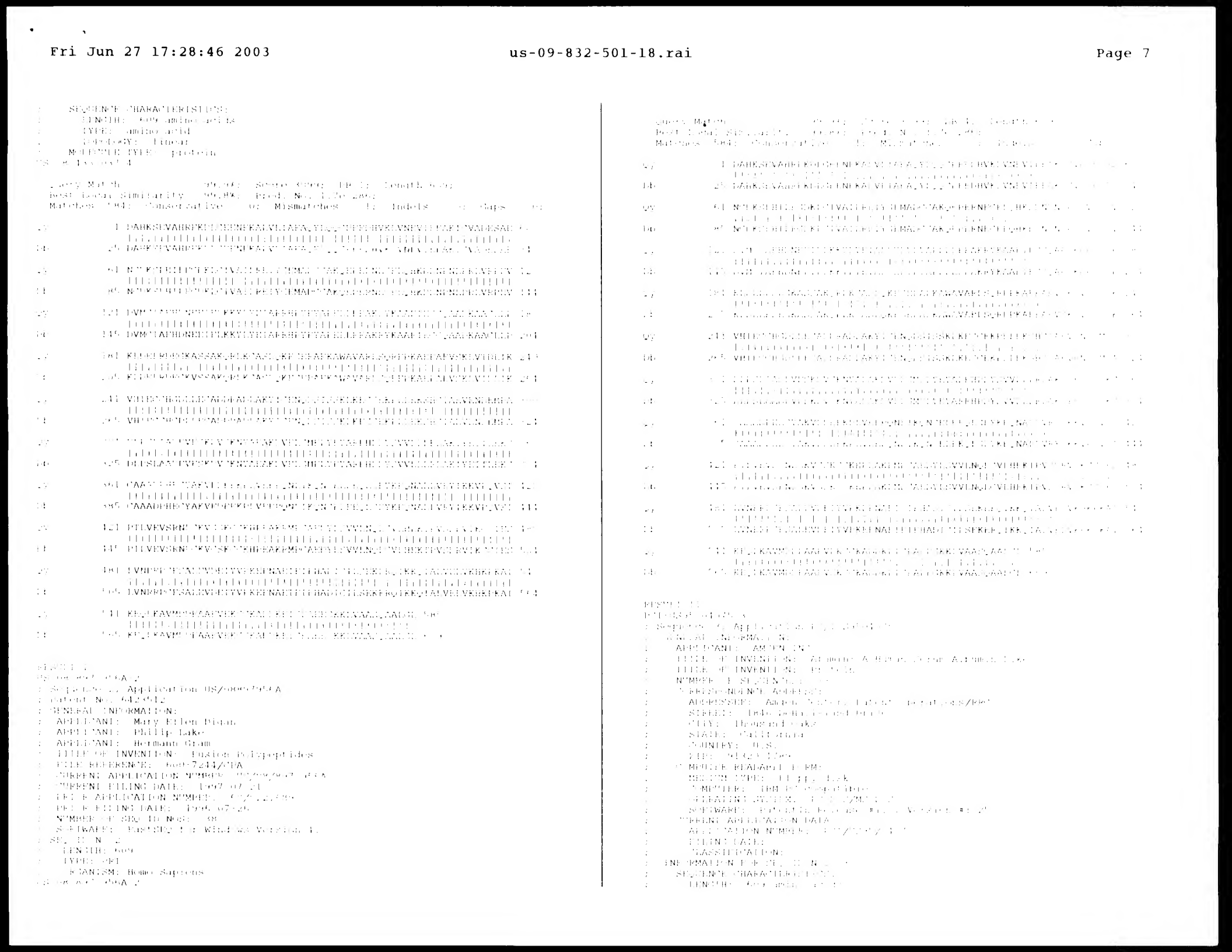
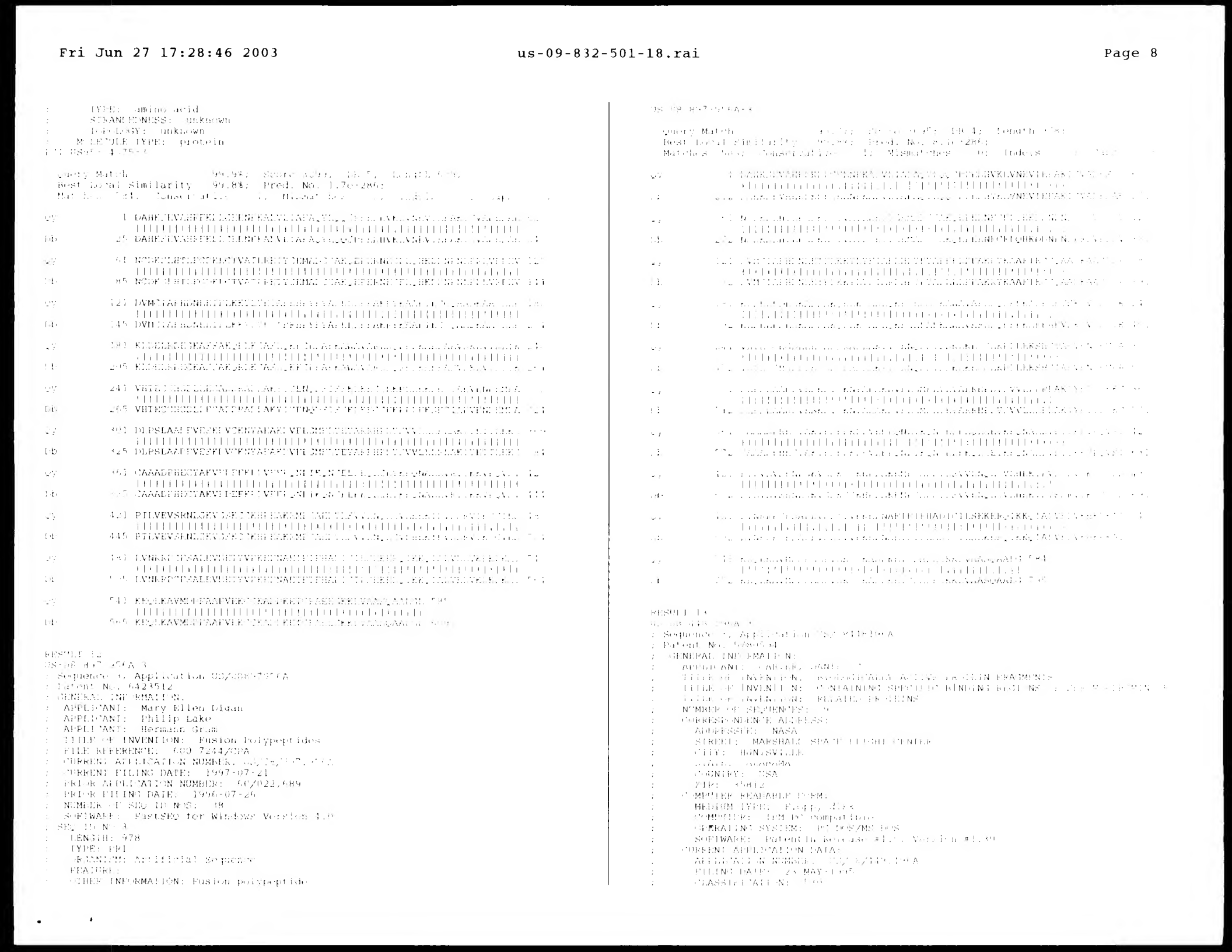
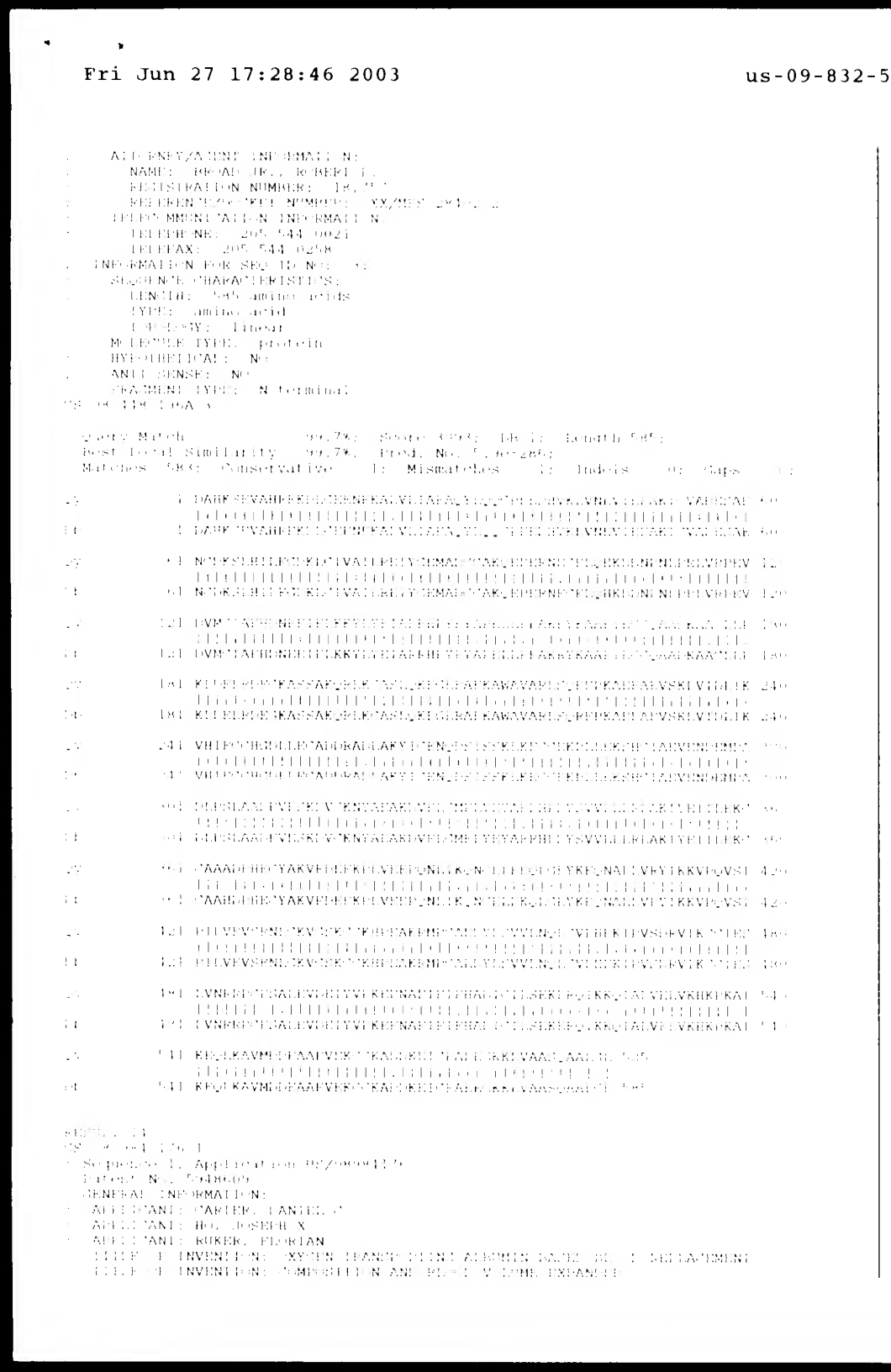
; Sequence 4, Application US/08433037
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Stoekenius, Kathrynjohn
; APPLICANT: Barr, Kechia A.
; APPLICANT: Peterson, Russell A.
; APPLICANT: Infil, Steven L.
; APPLICANT: Ischoppe, Daniel E.
; TITLE OF INVENTION: EXPRESSION OF HUMAN ARROM ALBUMIN IN
; TITLE OF INVENTION: TRANSGENIC PLANTS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530-2020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,037
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Epstein, Edward S.
; REGISTRATION NUMBER: 31,847
; REFERENCE/DOCKET NUMBER: 412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 1:







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;   COMPUTER READABLE FORM:
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;     COMPUTER: IBM PC compatible
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;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/448,196A
;     FILING DATE: 23-MAY-1995
;     CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;     NAME: BROAD JR., ROBERT L.
;     REGISTRATION NUMBER: 18,757
;     REFERENCE/DOCKET NUMBER: AA/MBJ 23402-2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 205-544-0021
;     TELEFAX: 205-544-0258
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 583 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: N-terminal
US-08-448-196A-5

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  Best Local Similarity   75.8%;  Pred. No. 1.5e-225;
  Matches  442;  Conservative   70;  Mismatches   70;  Indels    1;  Gaps    1;

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Qy         61 [illegible] 120
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Qy        121 [illegible] 180
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GenCore version 5.1.4
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

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Scoring table: BLOSUM62
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Searched:      424697 seqs, 10064083 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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  Pred. No. is the number of results predicted by chance to have a
  score greater than or equal to the score of the result being printed,
  and is derived by analysis of the total score distribution.
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SUMMARIES

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2	3103	100.0	585	9	US-09-984-[illegible]-26	Sequence 26, Appl
3	3103	100.0	585	10	US-09-929-[illegible]-2	Sequence 2, Appli
4	3103	100.0	585	12	US-10-153-064-[illegible]	Sequence 5, Appli
5	3103	100.0	601	9	US-09-984-[illegible]	Sequence 7, Appli
6	3103	100.0	609	9	US-[illegible]	Sequence 370, App
7	3103	100.0	609	12	US-10-153-064-[illegible]	Sequence 7, Appli
8	3103	100.0	610	9	US-10-237-667-2	Sequence 2, Appli
9	3103	100.0	610	9	US-10-237-[illegible]-2	Sequence 2, Appli
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16	3103	100.0	653	12	US-10-153-064-131	Sequence 131, App
17	3103	100.0	656	12	US-10-153-064-130	Sequence 130, App
18	3103	100.0	676	12	US-10-153-064-127	Sequence 127, App
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ALIGNMENTS

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; Sequence 445, Application US/0[illegible]
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; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  APPLICANT: Beck[illegible], James [illegible]
;  APPLICANT: Potter, M. [illegible]
;  APPLICANT: Fleming, [illegible]
;  APPLICANT: Rosen, [illegible] A.
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/0[illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn [illegible]
; SEQ ID NO 445
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-[illegible]-445

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  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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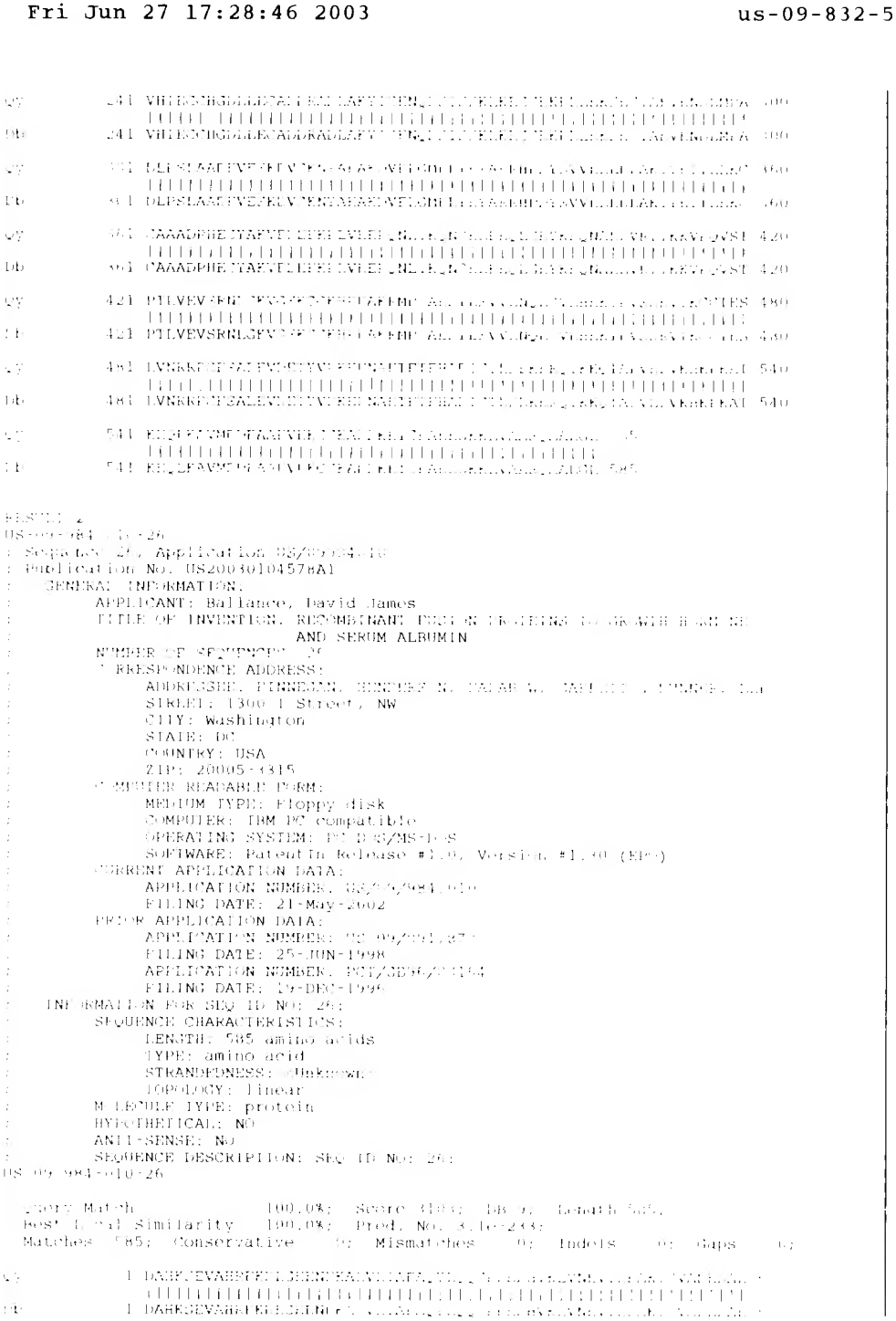

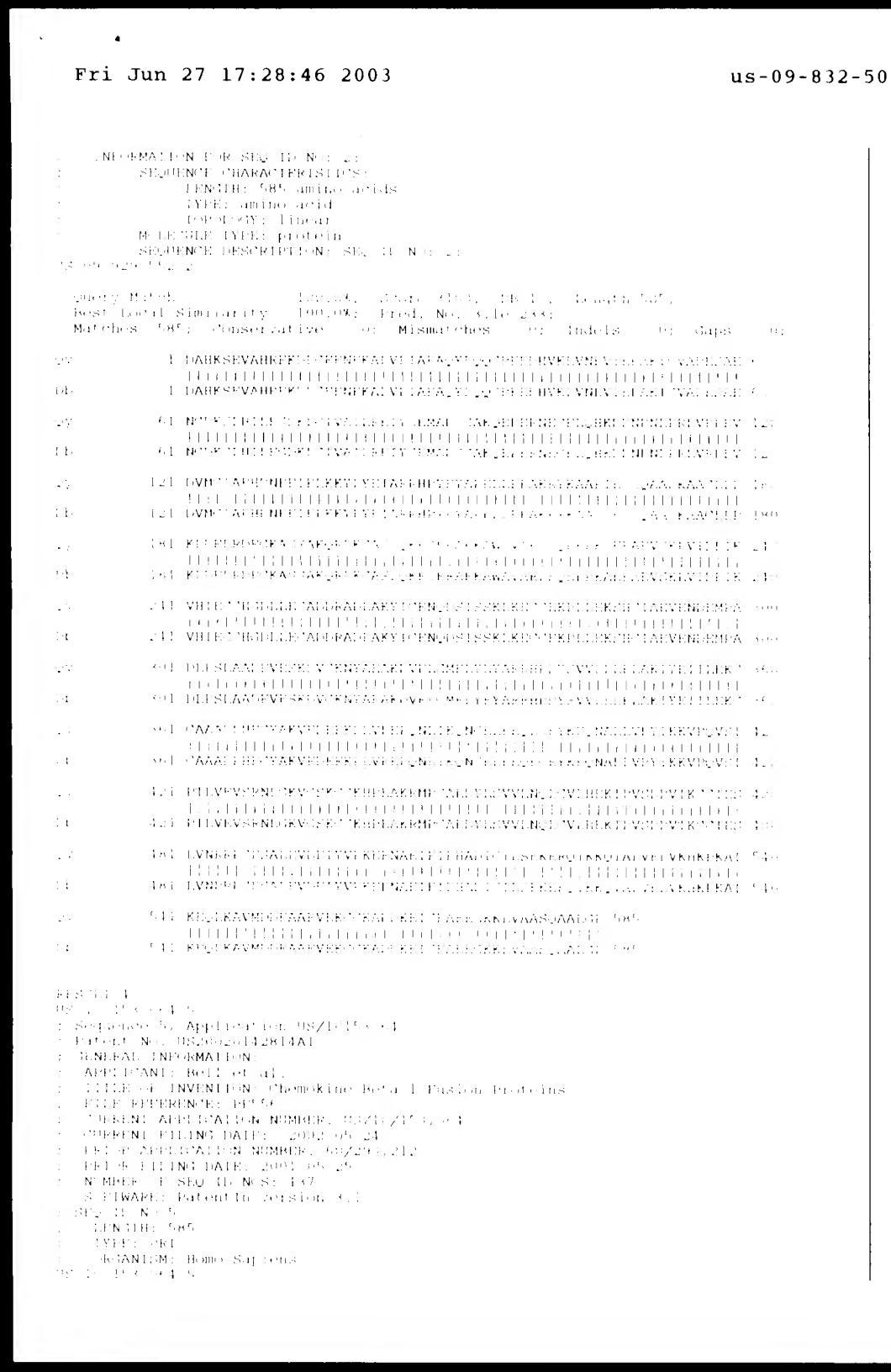

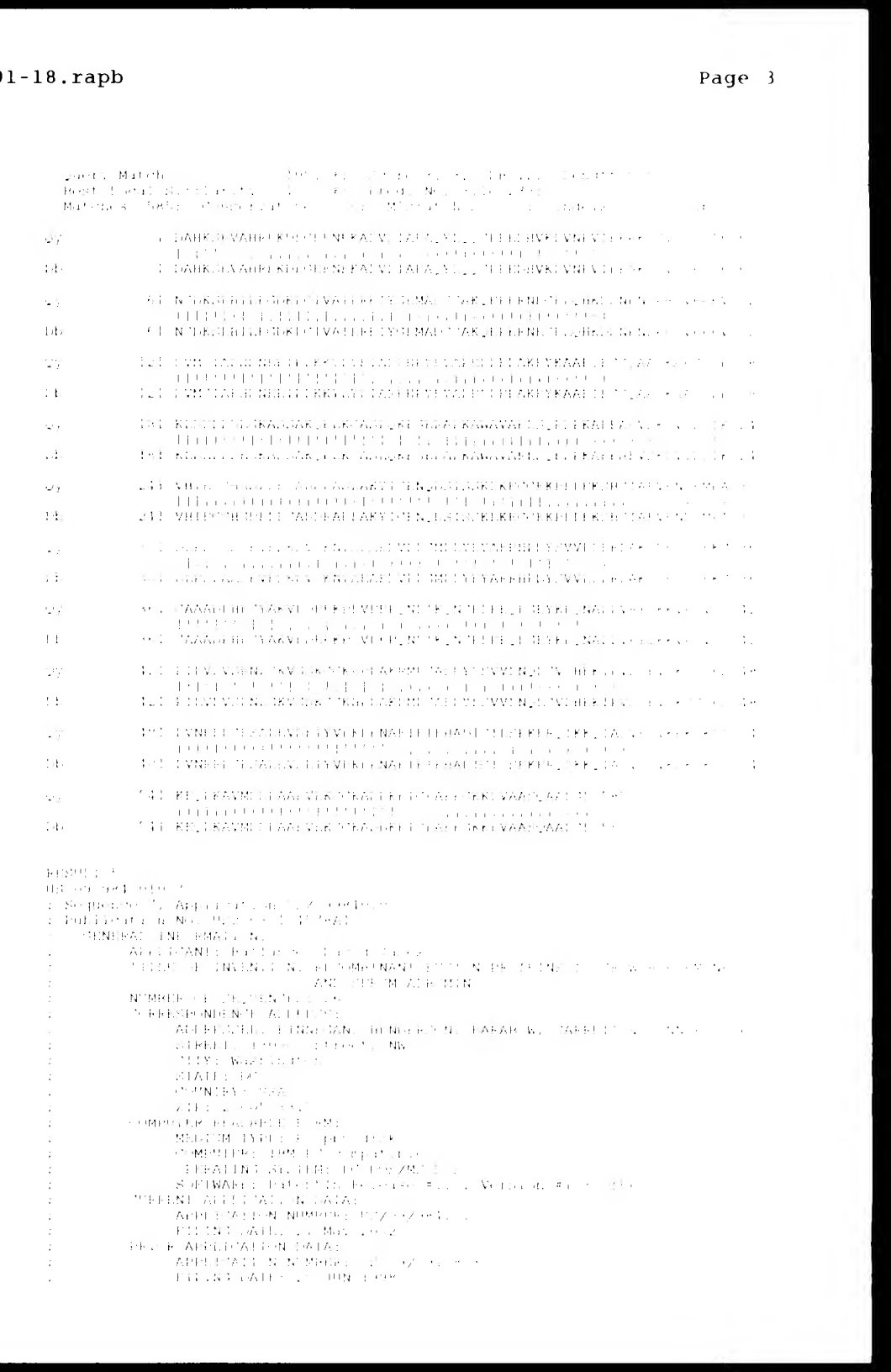

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;          FILING DATE: 19-DEC-1996
;   INFORMATION FOR SEQ ID NO: 7:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 604 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: unknown
;          TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      HYPOTHETICAL: NO
;      ANTI-SENSE: NO
;      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-084-810-7

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Db        320 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 379

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RESULT 6
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; Sequence 370, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 461
;  SOFTWARE: PERL Program
;  SEQ ID NO 370
;    LENGTH: 609
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    OTHER INFORMATION: Incyte ID No: [illegible]AI 000657[illegible]
US-09-919-039-370

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. 3.2e-233;
  Matches  585;  Conservative    0;  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

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Db        145 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 204

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Qy        241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
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Db        265 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 324

Qy        301 DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
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Db        385 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 444

Qy        421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
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Qy        481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
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RESULT 7
US-10-153-064-7
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; Patent No. US[illegible]114281A1
; GENERAL INFORMATION:
;  APPLICANT: Bell et al.
;  TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
;  FILE REFERENCE: PF556
;  CURRENT APPLICATION NUMBER: US/10/153,064
;  CURRENT FILING DATE: 2002-05-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
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US-10-153-064-7
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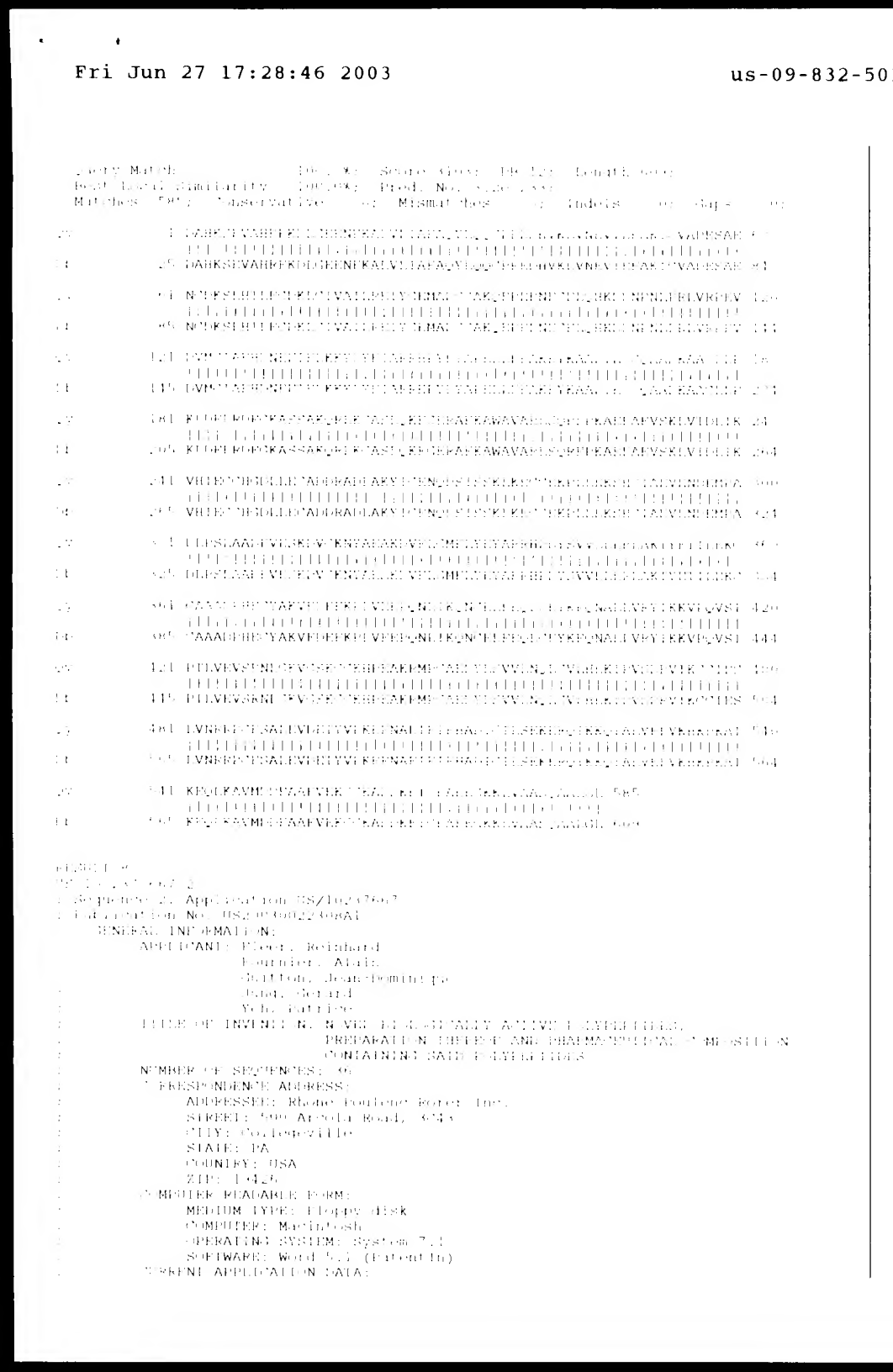

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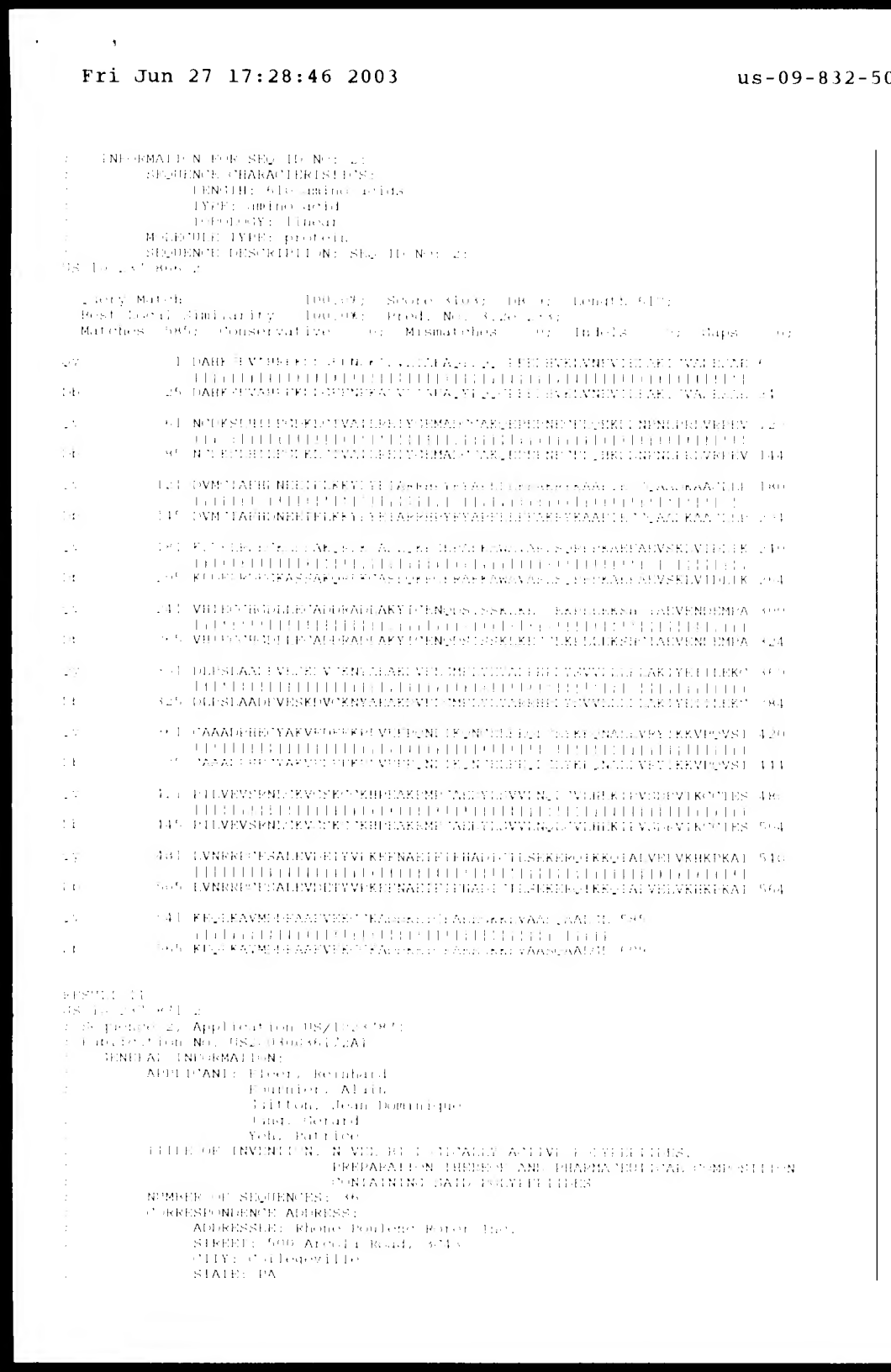
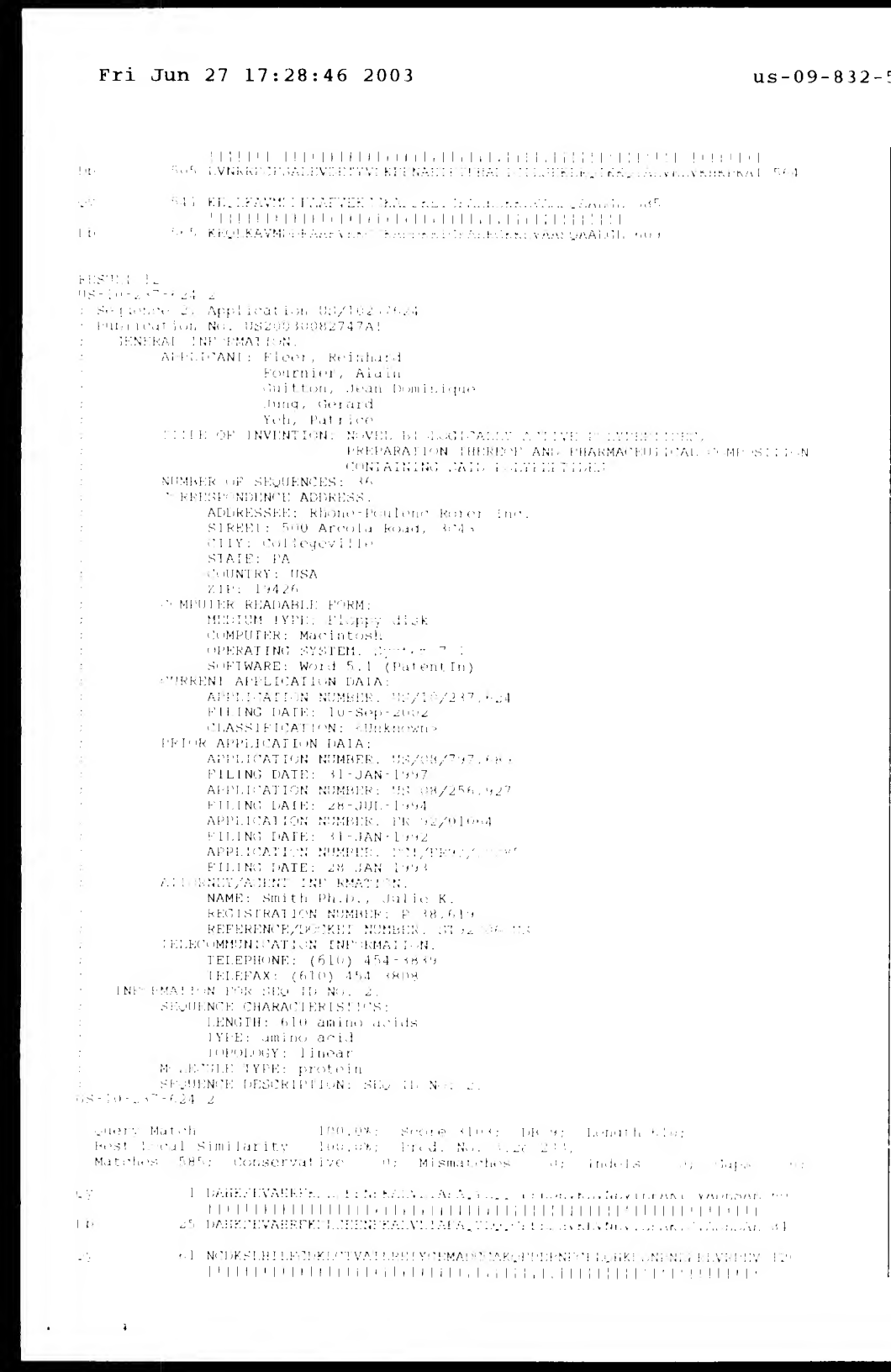
; Sequence 2, Application US/09237708
; Publication No. US20030036170A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jund, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3048
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/237,708
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: 530Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00065
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julia K.
; REGISTRATION NUMBER: P 38,619
; REFERENCE/DOCKET NUMBER: SF2006 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-4839
; TELEFAX: (610) 454-4808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-237-708-2

Query Match 100.0%; Score 3193; DB 0; Length 616;
Best Local Similarity 100.0%; Pred. No. 1.2e-243;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-237-708-2
; Sequence 2, Application US/09237708
; Publication No. US20030036170A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jund, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3048
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/237,708
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: 530Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00065
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julia K.
; REGISTRATION NUMBER: P 38,619
; REFERENCE/DOCKET NUMBER: SF2006 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-4839
; TELEFAX: (610) 454-4808





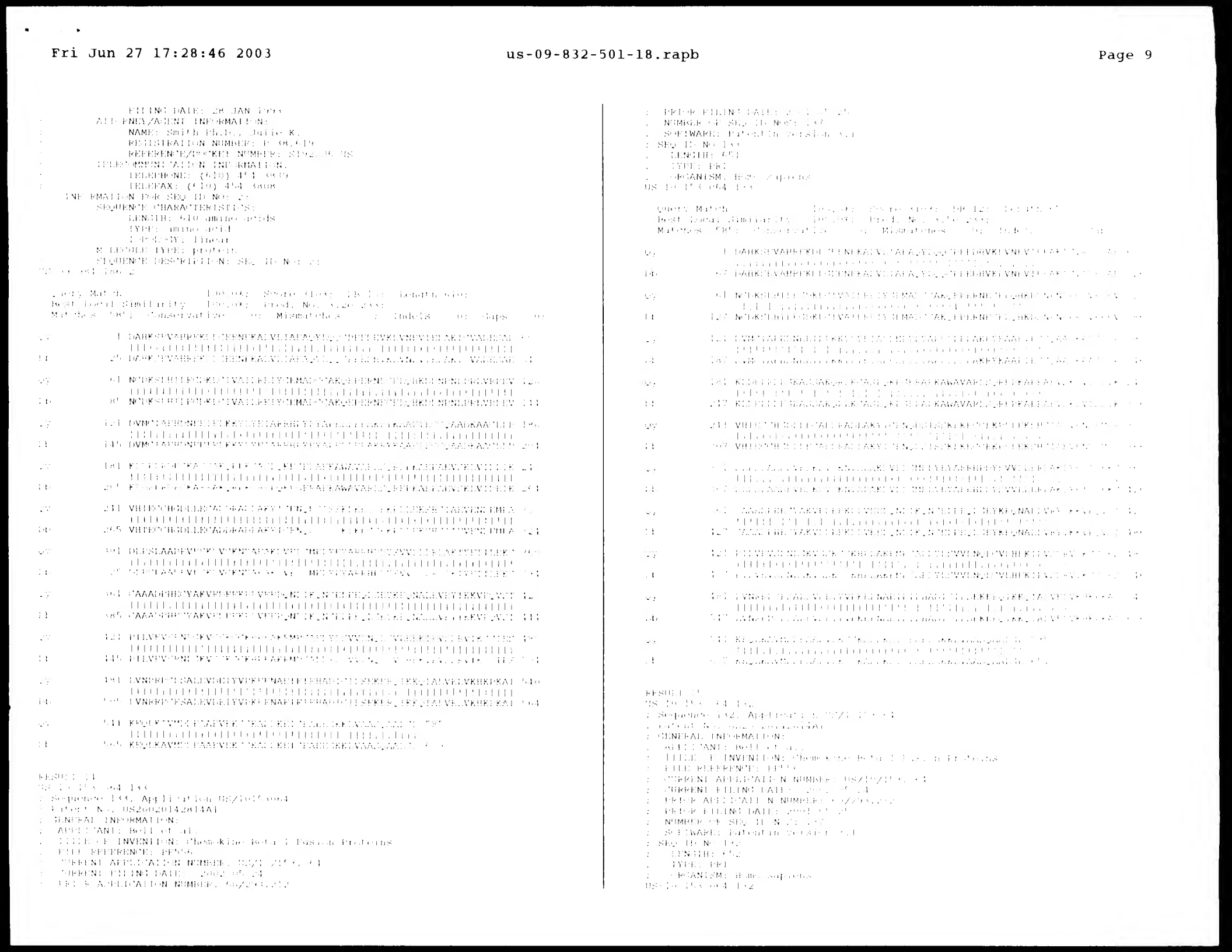
RESULT 1
US-09-832-501-24
; Sequence 24, Application US/09832747A
; Publication No. US20030082747A1
; GENERAL INFORMATION:
; APPLICANT: Floer, Reinhard
; Fournier, Alain
; Guitton, Jean Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 30th
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,747
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,884
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01004
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: US/07/824,[illegible]
; FILING DATE: 28 JAN 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P 38,619
; REFERENCE/DOCKET NUMBER: GT-22-36.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3809
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-832-501-24

Query Match 100.0%; Score 5105; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.2e-235;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24
US-09-832-501-2
; Sequence 2, Application US/09832747A
; Publication No. US20030082747A1
; GENERAL INFORMATION:
; APPLICANT: Floer, Reinhard
; Fournier, Alain
; Guitton, Jean Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 30th
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,747
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,884
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01004
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: US/07/824,[illegible]
; FILING DATE: 28 JAN 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P 38,619
; REFERENCE/DOCKET NUMBER: GT-22-36.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3809
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-832-501-2



Query Match 102.0%; Score 3103; DB 12; Length 652;
Best Local Similarity 100.0%; Pred. No. 3.5e-233;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: June 27, 2003, 17:15:40
Total time : 28 secs